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(54) Title: RECEPTOR OF THE THYROID/STEROID HORMONE RECEPTOR SUPERFAMILY

(57) Abstract

Novel members of the steroid/thyroid superfamily of receptors are described. DNA sequences encoding same, expression vectors containing such DNA and host cells transformed with such expression vectors are also disclosed, as are methods for the expression of the novel receptors of the invention, and various uses thereof.

RECEPTOR OF THE THYROID/STEROID HORMONE RECEPTOR SUPERFAMILY

FIELD OF THE INVENTION

The present invention relates to novel steroid-hormone or steroid-hormone like receptor proteins, genes encoding such proteins, and methods of making and using such proteins. In a particular aspect, the present invention relates to bioassay systems for determining the selectivity of interaction between ligands and steroid-hormone or steroid-hormone like receptor proteins.

10

BACKGROUND OF THE INVENTION

Transcriptional regulation of development and homeostasis in complex eukaryotes, including humans and other mammals, birds, fish, insects, and the like, is controlled by a wide variety of regulatory substances, including steroid and thyroid hormones. These hormones exert potent effects on development and differentiation of phylogenetically diverse organisms. The effects of hormones are mediated by interaction with specific, high affinity binding proteins referred to as receptors.

The ability to identify additional compounds which are able to affect transcription of genes which are responsive to steroid hormones or metabolites thereof, would be of significant value in identifying compounds of potential therapeutic use. Further, systems useful for monitoring solutions, body fluids, and the like, for the presence of steroid hormones or metabolites thereof, would be of value in medical diagnosis, as well as for various biochemical applications.

A number of receptor proteins, each specific for one of several classes of cognate steroid hormones [e.g., estrogens (estrogen receptor), progesterones (progesteron

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receptor), glucocorticoid (glucocorticoid receptor), androgens (androgen receptor), aldosterones (mineralocorticoid receptor), vitamin D (vitamin D receptor)], retinoids (e.g., retinoic acid receptor) or for
5 cognate thyroid hormones (e.g., thyroid hormone receptor), are known. Receptor proteins have been found to be distributed throughout the cell population of complex eukaryotes in a tissue specific fashion.

10 Molecular cloning studies have made it possible to demonstrate that receptors for steroid, retinoid and thyroid hormones are all structurally related and comprise a superfamily of regulatory proteins. These regulatory proteins are capable of modulating specific gene expression
15 in response to hormone stimulation by binding directly to cis-acting elements. Structural comparisons and functional studies with mutant receptors have revealed that these molecules are composed of a series of discrete functional domains, most notably, a DNA-binding domain that is
20 composed typically of 66-68 amino acids, including two zinc fingers and an associated carboxy terminal stretch of approximately 250 amino acids, which latter region comprises the ligand-binding domain.

25 An important advance in the characterization of this superfamily of regulatory proteins has been the delineation of a growing list of gene products which possess the structural features of hormone receptors. This growing list of gene products has been isolated by low-
30 stringency hybridization techniques employing DNA sequences encoding previously identified hormone receptor proteins.

It is known that steroid or thyroid hormones, protected forms thereof, or metabolites thereof, enter
35 cells and bind to the corresponding specific receptor protein, initiating an allosteric alteration of the

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protein. As a result of this alteration, the complex of receptor and hormone (or metabolite thereof) is capable of binding to certain specific sites on chromatin with high affinity.

5

It is also known that many of the primary effects of steroid and thyroid hormones involve increased transcription of a subset of genes in specific cell types.

10

A number of steroid hormone- and thyroid hormone-responsive transcriptional control units have been identified. These include the mouse mammary tumor virus 5'-long terminal repeat (MTV LTR), responsive to glucocorticoid, aldosterone and androgen hormones; the transcriptional control units for mammalian growth hormone genes, responsive to glucocorticoids, estrogens and thyroid hormones; the transcriptional control units for mammalian prolactin genes and progesterone receptor genes, responsive to estrogens; the transcriptional control units for avian ovalbumin genes, responsive to progestones; mammalian metallothionein gene transcriptional control units, responsive to glucocorticoids; and mammalian hepatic α_2 -globulin gene transcriptional control units, responsive to androgens, estrogens, thyroid hormones, and glucocorticoids.

25

A major obstacle to further understanding and more widespread use of the various members of the steroid/thyroid superfamily of hormone receptors has been a lack of availability of the receptor proteins, in sufficient quantity and sufficiently pure form, to allow them to be adequately characterized. The same is true for the DNA gene segments which encode them. Lack of availability of these DNA segments has prevented in vitro manipulation and in vivo expression of the receptor-

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encoding genes, and consequently the knowledge such manipulation and expression would yield.

In addition, a further obstacle to a more
5 complete understanding and more widespread use of members of the steroid/thyroid receptor superfamily is the fact that additional members of this superfamily remain to be discovered, isolated and characterized.

10 The present invention is directed to overcoming these problems of short supply of adequately purified receptor material, lack of DNA segments which encode such receptors and increasing the number of identified and
15 characterized hormone receptors which are available for use.

BRIEF DESCRIPTION OF THE INVENTION

In accordance with the present invention, we have
20 discovered novel members of the steroid/thyroid superfamily of receptors. The novel receptors of the present invention are soluble, intracellular, nuclear (as opposed to cell surface) receptors, which are activated to modulate transcription of certain genes in animal cells when the
25 cells are exposed to ligands therefor. The nuclear receptors of the present invention differ significantly from known steroid receptors, both in primary sequence and in responsiveness to exposure of cells to various ligands, e.g., steroids or steroid-like compounds.

30

Also provided in accordance with the present invention are DNAs encoding the receptors of the present invention, including expression vectors for expression thereof in animal cells, cells transformed with such
35 expression vectors, cells co-transformed with such expression vectors and reporter vectors (to monitor the

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ability of the receptors to modulate transcription when the cells are exposed to a compound which interacts with the receptor); and methods of using such co-transformed cells in screening for compounds which are capable of leading to modulation of receptor activity.

Further provided in accordance with the present invention are DNA and RNA probes for identifying DNAs encoding additional steroid receptors.

10

In accordance with yet another embodiment of the invention, there is provided a method for making the receptors of the invention by expressing DNAs which encode the receptors in suitable host organisms.

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The novel receptors and DNAs encoding same can be employed for a variety of purposes. For example, novel receptors of the present invention can be included as part of a panel of receptors which are screened to determine the selectivity of interaction of proposed agonists or antagonists and other receptors. Thus, a compound which is believed to interact selectively, for example, with the glucocorticoid receptor, should not have any substantial effect on any other receptors, including those of the present invention. Conversely, if such a proposed compound does interact with one or more of the invention receptors, then the possibility of side reactions caused by such compound is clearly indicated.

30

BRIEF DESCRIPTION OF THE FIGURE

Figure 1 is a schematic diagram correlating the relationship between the alternate spliced variants of invention receptor XR1.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, there are provided DNAs encoding a polypeptide characterized by having a DNA binding domain comprising about 66 amino acids with 9 cysteine (Cys) residues, wherein said DNA binding domain has:

- 10 (i) less than about 70% amino acid sequence identity with the DNA binding domain of human retinoic acid receptor-alpha (hRAR-alpha);
- (ii) less than about 60% amino acid sequence identity with the DNA binding domain of human thyroid receptor-beta (hTR-beta);
- 15 (iii) less than about 50% amino acid sequence identity with the DNA binding domain of human glucocorticoid receptor (hGR); and
- (iv) less than about 65% amino acid sequence identity in with the DNA binding domain of human retinoid X receptor-alpha (hRXR-alpha).
- 20

Alternatively, DNAs of the invention can be characterized with respect to percent amino acid sequence identity of the ligand binding domain of polypeptides encoded thereby, relative to amino acid sequences of previously characterized receptors. As yet another alternative, DNAs of the invention can be characterized by the percent overall amino acid sequence identity of polypeptides encoded thereby, relative to amino acid sequences of previously characterized receptors.

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Thus, DNAs of the invention can be characterized as encoding polypeptides having, in the ligand binding domain:

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- (i) less than about 35% amino acid sequence identity with the ligand binding domain of hRAR-alpha;
- 5 (ii) less than about 30% amino acid sequence identity with the ligand binding domain of hTR-beta;
- (iii) less than about 25% amino acid sequence identity with the ligand binding domain of hGR; and
- 10 (iv) less than about 30% amino acid sequence identity with the ligand binding domain of hRXR-alpha.

DNA's of the invention can be further characterized as encoding polypeptides having an overall amino acid sequence identity of:

15

- (i) less than about 35% relative to hRAR-alpha;
- (ii) less than about 35% relative to hTR-beta;
- 20 (iii) less than about 25% relative to hGR; and
- (iv) less than about 35% relative to hRXR-alpha.

25

Specific receptors contemplated for use in the practice of the present invention include:

"XR1" (variously referred to herein as receptor "XR1", "hXR1", "hXR1.pep" or "verHT19.pep"; wherein the prefix "h" indicates the clone is of human origin), a polypeptide characterized as having a DNA binding domain comprising:

30

- (i) about 68% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- 35

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(ii) about 59% amino acid sequence identity with the DNA binding domain of hTR-beta;

(iii) about 45% amino acid sequence identity with the DNA binding domain of hGR; and

(iv) about 65% amino acid sequence identity with the DNA binding domain of hRXR-alpha;

see also Sequence ID No. 2 for a specific amino acid sequence representative of XR1, as well as Sequence ID No. 1 which is an exemplary nucleotide sequence encoding XR1. In addition, Sequence ID Nos. 4 and 6 present alternate amino terminal sequences for the clone referred to as XR1 (the variant referred to as verht3 is presented in Sequence ID No. 4 (an exemplary nucleotide sequence encoding such variant presented in Sequence ID No. 3), and the variant referred to as verhr5 is presented in Sequence ID No. 6 (an exemplary nucleotide sequence encoding such variant presented in Sequence ID No. 5);

"XR2" (variously referred to herein as receptor "XR2", "hXR2" or "hXR2.pep"), a polypeptide characterized as having a DNA binding domain comprising:

(i) about 55% amino acid sequence identity with the DNA binding domain of hRAR-alpha;

(ii) about 56% amino acid sequence identity with the DNA binding domain of hTR-beta;

(iii) about 50% amino acid sequence identity with the DNA binding domain of hGR; and

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- (iv) about 52% amino acid sequence identity with the DNA binding domain of hRXR-alpha;

5 see also Sequence ID No. 8 for a specific amino acid sequence representative of XR2, as well as Sequence ID No. 7 which is an exemplary nucleotide sequence encoding XR2;

10 "XR4" (variously referred to herein as receptor "XR4", "mXR4" or "mXR4.pep"; wherein the prefix "m" indicates the clone is of mouse origin), a polypeptide characterized as having a DNA binding domain comprising:

- 15 (i) about 62% amino acid sequence identity with the DNA binding domain of hRAR-alpha;

- (ii) about 58% amino acid sequence identity with the DNA binding domain of hTR-beta;

- 20 (iii) about 48% amino acid sequence identity with the DNA binding domain of hGR; and

- (iv) about 62% amino acid sequence identity with the DNA binding domain of hRXR-alpha;

25 see also Sequence ID No. 10 for a specific amino acid sequence representative of XR4, as well as Sequence ID No. 9 which is an exemplary nucleotide sequence encoding XR4;

30 "XR5" (variously referred to herein as receptor "XR5", "mXR5" or "mXR5.pep"), a polypeptide characterized as having a DNA binding domain comprising:

- 35 (i) about 59% amino acid sequence identity with the DNA binding domain of hRAR-alpha;

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(ii) about 52% amino acid sequence identity with the DNA binding domain of hTR-beta;

(iii) about 44% amino acid sequence identity with the DNA binding domain of hGR; and

(iv) about 61% amino acid sequence identity with the DNA binding domain of hRXR-alpha;

see also Sequence ID No. 12 for a specific amino acid sequence representative of XR5, as well as Sequence ID No. 11 which is an exemplary nucleotide sequence encoding XR5; and

"XR79" (variously referred to herein as "XR79", "dXR79" or "dXR79.pep"; wherein the prefix "d" indicates the clone is of Drosophila origin), a polypeptide characterized as having a DNA binding domain comprising:

(i) about 59% amino acid sequence identity with the DNA binding domain of hRAR-alpha;

(ii) about 55% amino acid sequence identity with the DNA binding domain of hTR-beta;

(iii) about 50% amino acid sequence identity with the DNA binding domain of hGR; and

(iv) about 65% amino acid sequence identity with the DNA binding domain of hRXR-alpha;

see also Sequence ID No. 14 for a specific amino acid sequence representative of XR79, as well as Sequence ID No. 13 which is an exemplary nucleotide sequence encoding XR79.

The receptor referred to herein as "XR1" is observed as three closely related proteins, presumably

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produced by alternate splicing from a single gene. The first of these proteins to be characterized (referred to as "verht19") comprises about 548 amino acids, and has a M_r of about 63 kilodalton. Northern analysis indicates that a single mRNA species corresponding to XR1 is highly expressed in the brain. A variant of verht19 (alternatively referred to as "verht3", XR1' or XR1prim) is further characterized as comprising about 556 amino acids, and having a M_r of about 64 kilodalton. Yet another variant of verht19 (alternatively referred to as "verhr5", XR1'' or XR1prim2) is further characterized as comprising about 523 amino acids, and having a M_r of about 60 kilodalton. The interrelationship between these three variants of XR1 is illustrated schematically in Figure 1.

15

The receptor referred to herein as "XR2" is further characterized as a protein comprising about 440 amino acids, and having a M_r of about 50 kilodalton. Northern analysis indicates that a single mRNA species (~1.7 kb) corresponding to XR2 is expressed most highly in liver, kidney, lung, intestine and adrenals of adult male rats. Transactivation studies (employing chimeric receptors containing the XR2 DNA binding domain and the ligand binding domain of a prior art receptor) indicate that XR2 is capable of binding to TRE_{pal} . In terms of amino acid sequence identity with prior art receptors, XR2 is most closely related to the vitamin D receptor (39% overall amino acid sequence identity, 17% amino acid identity in the amino terminal domain of the receptor, 53% amino acid identity in the DNA binding domain of the receptor and 37% amino acid identity in the ligand binding domain of the receptor).

The receptor referred to herein as "XR4" is further characterized as a protein comprising about 439 amino acids, and having a M_r of about 50 kilodalton. In

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terms of amino acid sequence identity with prior art receptors, XR4 is most closely related to the peroxisome proliferator-activated receptor (62% overall amino acid sequence identity, 30% amino acid identity in the amino terminal domain of the receptor, 86% amino acid identity in the DNA binding domain of the receptor and 64% amino acid identity in the ligand binding domain of the receptor). XR4 is expressed ubiquitously and throughout development (as determined by in situ hybridization).

10

The receptor referred to herein as "XR5" is further characterized as a protein comprising about 556 amino acids, and having a M_r of about 64 kilodalton. In situ hybridization reveals widespread expression throughout development. High levels of expression are observed in the embryonic liver around day 12, indicating a potential role in haematopoiesis. High levels are also found in maturing dorsal root ganglia and in the skin. In terms of amino acid sequence identity with prior art receptors, XR5 is most closely related to the rat nerve growth factor induced protein-B (NGFI-B) receptor. With respect to NGFI-B, XR5 has 29% overall amino acid sequence identity, 15% amino acid identity in the amino terminal domain of the receptor, 52% amino acid identity in the DNA binding domain of the receptor and 29% amino acid identity in the ligand binding domain of the receptor.

The receptor referred to herein as "XR79" is further characterized as a protein comprising about 601 amino acids, and having a M_r of about 66 kilodalton. Whole mount in situ hybridization reveals a fairly uniform pattern of RNA expression during embryogenesis. Northern blot analysis indicates that a 2.5 kb transcript corresponding to XR79 is present in RNA throughout development. The levels of XR79 mRNA are highest in RNA from 0 - 3 hour old embryos, i.e., maternal product, and

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lowest in RNA from the second instar larvae (L2 stage). In situ hybridization reveals that XR79 is distributed relatively uniformly at different stages of embryogenesis. In terms of amino acid sequence identity with prior art

5 receptors, XR79 is most closely related to the mammalian receptor TR2 [see Chang and Kokontis in Biochemical and Biophysical Research Communications 155: 971-977 (1988)], as well as members of the coup family, i.e., ear2, coup(ear3), harp-1. With respect to TR2, XR79 has 33%

10 overall amino acid sequence identity, 16% amino acid identity in the amino terminal domain of the receptor, 74% amino acid identity in the DNA binding domain of the receptor and 28% amino acid identity in the ligand binding domain of the receptor. With respect to coup (ear3) [see

15 Miyajima et al., in Nucl Acids Res 16: 11057-11074 (1988)], XR79 has 32% overall amino acid sequence identity, 21% amino acid identity in the amino terminal domain of the receptor, 62% amino acid identity in the DNA binding domain of the receptor and 22% amino acid identity in the ligand

20 binding domain of the receptor.

In accordance with a specific embodiment of the present invention, there is provided an expression vector which comprises DNA as previously described (or functional

25 fragments thereof), and which further comprises:

at the 5'-end of said DNA, a promoter and a nucleotide triplet encoding a translational start codon, and

at the 3'-end of said DNA, a nucleotide

30 triplet encoding a translational stop codon;

wherein said expression vector is operative in a cell in culture (e.g., yeast, bacteria, mammalian) to express the protein encoded by said DNA.

35 As employed herein, reference to "functional fragments" embraces DNA encoding portions of the invention

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receptors which retain one or more of the functional characteristics of steroid hormone or steroid hormone-like receptors, e.g., DNA binding properties of such receptors, ligand binding properties of such receptors, the ability to heterodimerize, nuclear localization properties of such receptors, phosphorylation properties of such receptors, transactivation domains characteristic of such receptors, and the like.

10 In accordance with a further embodiment of the present invention, there are provided cells in culture (e.g., yeast, bacteria, mammalian) which are transformed with the above-described expression vector.

15 In accordance with yet another embodiment of the present invention, there is provided a method of making the above-described novel receptors (or functional fragments thereof) by culturing the above-described cells under conditions suitable for expression of polypeptide product.

20 In accordance with a further embodiment of the present invention, there are provided novel polypeptide products produced by the above-described method.

25 In accordance with a still further embodiment of the present invention, there are provided chimeric receptors comprising at least an amino-terminal domain, a DNA-binding domain, and a ligand-binding domain,

30 wherein at least one of the domains thereof is derived from the novel polypeptides of the present invention; and

35 wherein at least one of the domains thereof is derived from at least one previously identified member of the steroid/thyroid superfamily of receptors e.g., glucocorticoid receptor (GR), thyroid receptors (TR), retinoic

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acid receptors (RAR), mineralocorticoid receptor (MR), estrogen receptor (ER), the estrogen related receptors (e.g., hERR1 or hERR2), retinoid X receptors (e.g., RXR α , RXR β or RXR δ), vitamin D receptor (VDR), aldosterone receptor (AR), progesterone receptor (PR), the ultraspiracle receptor (USP), nerve growth factor induced protein-B (NGFI-B), the coup family of transcription factors (COUP), peroxisome proliferator-activated receptor (PPAR), mammalian receptor TR2 (TR2), and the like.

In accordance with yet another embodiment of the present invention, there is provided a method of using polypeptides of the invention to screen for response elements and/or ligands for the novel receptors described herein. The method to identify compounds which act as ligands for receptor polypeptides of the invention comprising:

assaying for the presence or absence of reporter protein upon contacting of cells containing a chimeric form of said receptor polypeptide and reporter vector with said compound;

wherein said chimeric form of said receptor polypeptide comprises the ligand binding domain of said receptor polypeptide and the amino-terminal and DNA-binding domains of one or more previously identified members of the steroid/thyroid superfamily of receptors;

wherein said reporter vector comprises:

- (a) a promoter that is operable in said cell,
- (b) a hormone response element which is responsive to the receptor from which the DNA-binding domain of said chimeric form of said receptor polypeptide is derived, and

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(c) a DNA segment encoding a reporter protein,

wherein said reporter protein-encoding DNA segment is operatively linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element is operatively linked to said promoter for activation thereof, and thereafter

identifying those compounds which induce or block the production of reporter in the presence of said chimeric form of said receptor polypeptide.

The method to identify response elements for receptor polypeptides of the invention comprises:

assaying for the presence or absence of reporter protein upon contacting of cells containing a chimeric form of said receptor polypeptide and reporter vector with a compound which is a known agonist or antagonist for the receptor from which the ligand-binding domain of said chimeric form of said receptor polypeptide is derived;

wherein said chimeric form of said receptor polypeptide comprises the DNA-binding domain of the receptor polypeptide and the amino-terminal and ligand-binding domains of one or more previously identified members of the steroid/thyroid superfamily of receptors;

wherein said reporter vector comprises:

(a) a promoter that is operable in said cell,

(b) a putative hormone response element, and

(c) a DNA segment encoding a reporter protein,

wherein said reporter protein-encoding DNA segment is operatively

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linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element is operatively linked to said promoter for activation thereof; and

identifying those response elements for which the production of reporter is induced or blocked in the presence of said chimeric form of said receptor polypeptide.

10

In accordance with yet another embodiment of the present invention, there is provided a DNA or RNA labeled for detection; wherein said DNA or RNA comprises a nucleic acid segment, preferably of at least 20 bases in length, wherein said segment has substantially the same sequence as a segment of the same length selected from the DNA segment represented by bases 21 - 1902, inclusive, of Sequence ID No. 1, bases 1 - 386, inclusive, of Sequence ID No. 3, bases 10 - 300, inclusive, of Sequence ID No. 5, bases 21 - 1615, inclusive, of Sequence ID No. 7, bases 21 - 2000, inclusive, of Sequence ID No. 9, bases 1 - 2450, inclusive, of Sequence ID No. 11, bases 21 - 2295, inclusive, of Sequence ID No. 13, or the complement of any of said segments.

25

In accordance with still another embodiment of the present invention, there are provided methods of testing compound(s) for the ability to regulate transcription-activating effects of a receptor polypeptide, said method comprising assaying for the presence or absence of reporter protein upon contacting of cells containing a receptor polypeptide and reporter vector with said compound;

wherein said receptor polypeptide is characterized by having a DNA binding domain comprising

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about 66 amino acids with 9 Cys residues, wherein said DNA binding domain has:

- 5 (i) less than about 70% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) less than about 60% amino acid sequence identity with the DNA binding domain of hTR-beta;
- 10 (iii) less than about 50% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) less than about 65% amino acid sequence identity with the DNA binding domain of hRXR-alpha; and

15 wherein said reporter vector comprises:

- (a) a promoter that is operable in said cell,
- (b) a hormone response element, and
- (c) a DNA segment encoding a reporter protein,

20 wherein said reporter protein-encoding DNA segment is operatively linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element is operatively linked to said promoter for activation thereof.

25 In accordance with a still further embodiment of the present invention, there is provided a method of testing a compound for its ability to selectively regulate the transcription-activating effects of a specific receptor polypeptide, said method comprising:

30 assaying for the presence or absence of reporter protein upon contacting of cells containing said receptor polypeptide and reporter vector with said compound;

wherein said receptor polypeptide is characterized by being responsive to the presence of a known ligand for said receptor to regulate the transcription of associated gene(s);

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wherein said reporter vector comprises:

- (a) a promoter that is operable in said cell,
- (b) a hormone response element, and
- (c) a DNA segment encoding a reporter protein,

wherein said reporter protein-encoding DNA segment is operatively linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element is operatively linked to said promoter for activation thereof; and

assaying for the presence or absence of reporter protein upon contacting of cells containing chimeric receptor polypeptide and reporter vector with said compound;

wherein said chimeric receptor polypeptide comprises the ligand binding domain of a novel receptor of the present invention, and the DNA binding domain of said specific receptor; and thereafter

selecting those compounds which induce or block the production of reporter in the presence of said specific receptor, but are substantially unable to induce or block the production of reporter in the presence of said chimeric receptor.

The above-described methods of testing compounds for the ability to regulate transcription-activating effects of invention receptor polypeptides can be carried out employing methods described in USSN 108,471, filed October 20, 1987, the entire contents of which are hereby incorporated by reference herein.

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As employed herein, the term "expression vector" refers to constructs containing DNA of the invention (or functional fragments thereof), plus all sequences necessary for manipulation and expression of such DNA. Such an expression vector will contain both a "translational start site" and a "translational stop site". Those of skill in the art can readily identify sequences which act as either translational start sites or translational stop sites.

10 Suitable host cells for use in the practice of the present invention include prokaryotic and eukaryote cells, e.g., bacteria, yeast, mammalian cells and the like.

15 Labeled DNA or RNA contemplated for use in the practice of the present invention comprises nucleic acid sequences covalently attached to readily analyzable species such as, for example, radiolabel (e.g., ^{32}P , ^3H , ^{35}S , and the like), enzymatically active label, and the like.

20 The invention will now be described in greater detail by reference to the following non-limiting examples.

EXAMPLES

EXAMPLE I

25 ISOLATION AND CHARACTERIZATION OF XR1

 The KpnI/SacI restriction fragment (503bp) including the DNA-binding domain of hRAR-alpha-encoding DNA
30 [See Giguere et al., Nature 330: 624-629 (1987); and commonly assigned United States Patent Application Serial No. 276,536, filed November 30, 1988; and European Patent Application Publication No. 0 325 849, all incorporated herein by reference] was nick-translated and used to screen
35 a rat brain cDNA library [see DNA Cloning, A practical approach, Vol I and II, D. M. Glover, ed. (IRL Press

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(1985)] and a lambda-gt11 human liver cDNA library [Kwok et al., Biochem. 24: 556 (1985)] at low stringency. The hybridization mixture contained 35% formamide, 1X Denhardt's, 5X SSPE (1X SSPE=0.15 M NaCl, 10mM Na₂HPO₄, 1mM EDTA), 0.1% SDS, 10% dextran sulfate, 100 µg/ml denatured salmon sperm DNA and 10⁶ cpm of [³²P]-labelled probe. Duplicate nitrocellulose filters were hybridized for 16h at 42°C, washed once at 25°C for 15 min with 2X SSC (1X SSC=0.15 M NaCl, 0.015 M sodium citrate), 0.1% SDS and then washed twice at 55°C for 30 min. in 2X SSC, 0.1% SDS. The filters were autoradiographed for 3 days at -70°C using an intensifying screen.

After several rounds of screening, a pure positive clone having an insert of about 2.1 kb is obtained from the rat brain cDNA library. Several positive clones are obtained from the human liver library. Sequence analysis of the positive rat brain clone indicates that this clone encodes a novel member of the steroid/thyroid superfamily of receptors. Sequence analysis of one of the positive human liver clones (designated "hL1", a 1.7 kb cDNA) indicates that this clone is the human equivalent of the rat brain clone, based on sequence homology.

The EcoRI insert of clone hL1 (labeled with ³²P) is also used as a probe to screen a human testis cDNA library (Clontech) and a human retina cDNA library [see Nathans et al., in Science 232: 193-202 (1986)]. Hybridization conditions comprised a hybridization mixture containing 50% formamide, 1X Denhardt's, 5X SSPE, 0.1% SDS, 100 µg/ml denatured salmon sperm DNA and 10⁶ cpm of [³²P]-labelled probe. Duplicate nitrocellulose filters were hybridized for 16h at 42°C, washed once at 25°C for 15 min with 2X SSC (1X SSC=0.15 M NaCl, 0.015 M sodium citrate), 0.1% SDS and then washed twice at 55°C for 30 min. in 2X

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SSC, 0.1% SDS. The filters were autoradiographed for 3 days at -70°C using an intensifying screen.

After several rounds of screening, five (5) positive clones were obtained from the human retina cDNA library, and five (5) positive clones were obtained from the human testis cDNA library. Sequence analysis of two clones from the testis library indicates that these clones encode different isoforms of the same novel member of the steroid/thyroid superfamily of receptors (designated as "Verht19" and "Verht3"). Sequence analysis of one of the positive clones from the human retina library indicates that this clone is yet another isoform of the same novel member of the steroid/thyroid superfamily of receptors (designated "Verhr5"). The full length sequence of Verht19 is set forth herein as Sequence ID No. 1 (which includes an indication of where the splice site is for each of the variants, verht3 and verhr5). The amino-terminal sequence of verht3 and verhr5 are presented in Sequence ID Nos. 3 and 5, respectively. In addition, the interrelationship between each of these three isoforms is illustrated schematically in Figure 1.

EXAMPLE II

ISOLATION AND CHARACTERIZATION OF XR2

The KpnI/SacI restriction fragment (503bp) including the DNA-binding domain of hRAR-alpha-encoding DNA [See Giguere et al., Nature 330: 624 (1987); and commonly assigned United States Patent Application Serial No. 276,536, filed November 30, 1988; and European Patent Application Publication No. 0 325 849, all incorporated herein by reference] was nick-translated and used to screen a lambda-gt11 human liver cDNA library [Kwok et al., Biochem. 24: 556 (1985)] at low stringency. The hybridization mixture contained 35% formamide, 1X

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Denhardt's, 5X SSPE (1X SSPE=0.15 M NaCl, 10mM Na₂HPO₄, 1mM EDTA), 0.1% SDS, 10% dextran sulfate, 100 mg/ml denatured salmon sperm DNA and 10⁶ cpm of [³²P]-labelled probe.

Duplicate nitrocellulose filters were hybridized for 16h at 42°C, washed once at 25°C for 15 min with 2X SSC (1X SSC=0.15 M NaCl, 0.015 M sodium citrate), 0.1% SDS and then washed twice at 55°C for 30 min. in 2X SSC, 0.1% SDS. The filters were autoradiographed for 3 days at -70°C using an intensifying screen.

10

Positive clones were isolated, subcloned into pGEM vectors (Promega, Madison, Wisconsin, USA), restriction mapped, and re-subcloned in various sized restriction fragments into M13mp18 and M13mp19 sequencing vectors. DNA sequence was determined by the dideoxy method with Sequenase™ sequencing kit (United States Biochemical, Cleveland, Ohio, USA) and analyzed by University of Wisconsin Genetics Computer Group programs [Devereux et al., Nucl. Acids Res. 12, 387 (1984)]. Several clones of a unique receptor-like sequence were identified, the longest of which was designated lambda-HL1-1 (also referred to herein as XR2).

The DNA sequence of the resulting clone is set forth as Sequence ID No. 7.

EXAMPLE III

ISOLATION AND CHARACTERIZATION OF XR4

A clone which encodes a portion of the coding sequence for XR4 was isolated from a mouse embryonic library by screening under low stringency conditions (as described above).

The library used was a lambda gt10 day 8.5 cDNA library having an approximate titer of 1.3 x 10¹⁰/ml

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(derived from 8.5 day old embryonic material with as much of the amnion and extraembryonic tissues dissected away as possible). This library was prepared from poly A⁺ select d RNA (by oligo-dT priming), Gubler & Hoffman cloning methods
5 [Gene 25: 263 (1983)], and cloned into the EcoRI site of lambda gt10.

The probe used was a mixture of radioactively labeled DNA derived from the DNA binding regions of the
10 human alpha and beta retinoic acid receptors.

Positive clones were isolated, subcloned into pGEM vectors (Promega, Madison, Wisconsin, USA), restriction mapped, and re-subcloned in various sized
15 restriction fragments into M13mp18 and M13mp19 sequencing vectors. DNA sequence was determined by the dideoxy method with Sequenase[™] sequencing kit (United States Biochemical, Cleveland, Ohio, USA) and analyzed by University of Wisconsin Genetics Computer Group programs [Devereux
20 et al., Nucl. Acids Res. 12, 387 (1984)]. Several clones of a unique receptor-like sequence were identified, the longest of which was designated XR4.

The DNA sequence of the resulting clone is set
25 forth as Sequence ID No. 9.

EXAMPLE IV

ISOLATION AND CHARACTERIZATION OF XR5

30 A clone which encodes a portion of the coding sequence for XR5 was isolated from a mouse embryonic library by screening under low stringency conditions (as described above).

35 The library used was the same lambda gt10 day 8.5 cDNA library described in the preceding example.

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Similarly, the probe used was the same mixture of radioactively labeled DNA described in the preceding example.

5 Only one of the clones isolated corresponds to a portion of the coding region for XR5. A 0.7 kb EcoRI fragment of this clone (designated as No. II-17) was subcloned into the bluescript pksII-Vector. Partial sequence analysis of this insert fragment shows homology to
10 the DNA binding domain of the retinoic acid receptors.

 The EcoRI-insert was used to rescreen a second library (a mouse lambda ZAPII day 6.5 cDNA library, prepared as described below) under high stringency
15 conditions. A total of 21 phages were isolated and rescued into the psk-vector. Partial sequencing allowed inserts from 13 of these phages to be identified as having sequences which overlap with XR5 II-17. The clone with the longest single EcoRI-insert was sequenced, revealing an
20 open reading frame of 556 amino acids. This sequence was extended further upstream by 9bp from the furthest 5'-reaching clone.

 The DNA sequence of the resulting clone is set
25 forth as Sequence ID No. 11.

 The day 6.5 cDNA library, derived from 6.5 day old mouse embryonic material was prepared from poly A⁺ selected RNA (by oligo-dT priming), and cloned into the
30 EcoRI site of lambda gt10.

EXAMPLE V

ISOLATION AND CHARACTERIZATION OF XR79

35 The 550 bp BamHI restriction fragment, including the DNA-binding domain of mouse RAR-beta-encoding DNA (See

Hamada et al., Proc. Natl. Acad. Sci. 86: 8289 (1989); incorporated by reference herein) was nick-translated and used to screen a Lambda-ZAP cDNA library comprising a size selected *Drosophila* genomic library (~2-5 kb, EcoRI restricted) at low stringency. The hybridization mixture contained 35% formamide, 1X Denhardt's, 5X SSPE (1X SSPE=0.15 M NaCl, 10mM Na₂HPO₄, 1mM EDTA), 0.1% SDS, 10% dextran sulfate, 100 mg/ml denatured salmon sperm DNA and 10⁶ cpm of [³²P]-labelled probe. Duplicate nitrocellulose filters were hybridized for 16h at 42°C, washed once at 25°C for 15 min with 2X SSC (1X SSC=0.15 M NaCl, 0.015 M sodium citrate), 0.1% SDS and then washed twice at 55°C for 30 min. in 2X SSC, 0.1% SDS. The filters were autoradiographed for 3 days at -70°C using an intensifying screen.

After several rounds of screening, a pure positive clone having an insert of about 3.5 kb is obtained from the *Drosophila* genomic library. This genomic clone was then used to screen a *Drosophila* imaginal disc lambda gt10 cDNA library [obtained from Dr. Charles Zuker; see DNA Cloning, A practical approach, Vol I and II, D. M. Glover, ed. (IRL Press (1985))]. Hybridization conditions comprised a hybridization mixture containing 50% formamide, 1X Denhardt's, 5X SSPE, 0.1% SDS, 100 µg/ml denatured salmon sperm DNA and 10⁶ cpm of [³²P]-labelled probe. Duplicate nitrocellulose filters were hybridized for 16h at 42°C, washed once at 25°C for 15 min with 2X SSC (1X SSC=0.15 M NaCl, 0.015 M sodium citrate), 0.1% SDS and then washed twice at 55°C for 30 min. in 2X SSC, 0.1% SDS. The filters were autoradiographed for 3 days at -70°C using an intensifying screen.

Sequence analysis of the positive cDNA clone indicates that this clone encodes another novel member of the steroid/thyroid superfamily of receptors (designated

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"XR79", a 2.5 kb cDNA). See Sequence ID No. 13 for the DNA sequence of the resulting clone.

The 2.5 kb cDNA encoding XR79 was nick-translated and used as a probe for a nitrocellulose filter containing size-fractionated total RNA, isolated by standard methods from *Drosophila melanogaster* of different developmental stages. The probe hybridized to a 2.5 kb transcript which was present in RNA throughout development. The levels were highest in RNA from 0 - 3 hour old embryos and lowest in RNA from second instar larvae. The same 2.5 kb cDNA was nick translated using biotinylated nucleotides and used as a probe for in situ hybridization to whole *Drosophila* embryos [Tautz and Pfeifle, *Chromosoma* 98: 81-85 (1989)]. The RNA distribution appeared relatively uniform at different stages of embryogenesis.

EXAMPLE VI

SEQUENCE COMPARISONS OF INVENTION RECEPTORS

WITH hRAR α , hTR β , hGR, AND hRXR α

Amino acid sequences of XR1, hRAR-alpha (human retinoic acid receptor-alpha), hTR-beta (human thyroid hormone receptor-beta), hGR (human glucocorticoid receptor), and hRXR-alpha (human retinoid receptor-alpha) were aligned using the University of Wisconsin Genetics Computer Group program "Bestfit" (Devereux et al., supra). The percentage of amino acid identity between RX2 and the other receptors, i.e., in the 66 - 68 amino acid DNA binding domains and the ligand-binding domains, are summarized in Table 1 as percent amino acid identity.

TABLE 1
Percent amino acid identity between
receptor XR1 (verht19) and hRAR α , TRB, hGR, and hRXR α

5	Comparison receptor	Percent amino acid identity			
		Overall	N-term ¹	DNA-BD ²	Ligand-BD ³
	hGR	18	21	45	20
10	hTRB	31	14	59	30
	hRAR α	32	25	68	27
	hRXR α	29	15	65	22

¹"N-term" = amino terminal domain
²"DNA-BD" = receptor DNA binding domain
³"Ligand-BD" = receptor ligand binding domain

Similarly, the amino acid sequences of invention
 20 receptors XR2, XR4, XR5, and XR79 were compared with human
 RAR-alpha (hRAR α), human TR-beta (hTR β), human
 glucocorticoid (hGR) and human RXR-alpha (hRXR α). As done
 in Table 1, the percentage of amino acid identity between
 the invention receptors and the other receptors are
 25 summarized in Tables 2 - 5, respectively.

TABLE 2
Percent amino acid identity between
receptor XR2 and hRAR α , TRB, hGR, and hRXR α

30	Comparison receptor	Percent amino acid identity			
		Overall	N-term ¹	DNA-BD ²	Ligand-BD ³
	hGR	24	21	50	20
35	hTRB	31	19	56	29
	hRAR α	33	21	55	32
	hRXR α	27	19	52	23

¹"N-term" = amino terminal domain
²"DNA-BD" = receptor DNA binding domain
³"Ligand-BD" = receptor ligand binding domain

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TABLE 3
Percent amino acid identity between
receptor XR4 and hRAR α , TR β , hGR, and hRXR α

5	Comparison receptor	Percent amino acid identity			
		Overall	N-term ¹	DNA-BD ²	Ligand-BD ³
	hGR	25	24	48	21
10	hTR β	31	21	58	27
	hRAR α	32	22	62	29
	hRXR α	33	24	62	28

¹"N-term" = amino terminal domain

¹"DNA-BD" = receptor DNA binding domain

²"Ligand-BD" = receptor ligand binding domain

TABLE 4
Percent amino acid identity between
receptor XR5 and hRAR α , TR β , hGR, and hRXR α

20	Comparison receptor	Percent amino acid identity			
		Overall	N-term ¹	DNA-BD ²	Ligand-BD ³
	hGR	20	20	44	20
	hTR β	24	14	52	22
	hRAR α	27	19	59	19
30	hRXR α	29	17	61	27

¹"N-term" = amino terminal domain

²"DNA-BD" = receptor DNA binding domain

³"Ligand-BD" = receptor ligand binding domain

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TABLE 5
Percent amino acid identity between
receptor XR79 and hRAR α , TR β , hGR, and hRXR α

5	Comparison receptor	Percent amino acid identity			
		Overall	N-term ¹	DNA-BD ²	Ligand-BD ³
10	hGR	18	22	50	20
	hTR β	28	22	55	20
	hRAR α	24	14	59	18
	hRXR α	33	20	65	24

¹"N-term" = amino terminal domain

²"DNA-BD" = receptor DNA binding domain

³"Ligand-BD" = receptor ligand binding domain

While the invention has been described in detail
with reference to certain preferred embodiments thereof, it
will be understood that modifications and variations are
within the spirit and scope of that which is described and
claimed.

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SUMMARY OF SEQUENCES

Sequence ID No. 1 is a nucleotide sequence
encoding novel receptor of the present invention designated
5 as "hXR1".

Sequence ID No. 2 is the amino acid sequence
deduced from the nucleotide sequence set forth in Sequence
ID No. 1 (variously referred to herein as receptor "XR1",
10 "hXR1", "hXR1.pep" or "verHT19.pep").

Sequence ID No. 3 is a nucleotide sequence
encoding the amino-terminal portion of the novel receptor
of the present invention designated as "hXR1prime".
15

Sequence ID No. 4 is the amino acid sequence
deduced from the nucleotide sequence set forth in Sequence
ID No. 3 (variously referred to herein as receptor
"XR1prime", "hXR1prime", "hXR1prime.pep" or "verHT3.pep").
20

Sequence ID No. 5 is a nucleotide sequence
encoding the amino-terminal portion of the novel receptor
of the present invention designated as "hXR1prim2".

Sequence ID No. 6 is the amino acid sequence
deduced from the nucleotide sequence set forth in Sequence
ID No. 5 (variously referred to herein as receptor
"XR1prim2", "hXR1prim2", "hXR1prim2.pep" or "verHr5.pep").
25

Sequence ID No. 7 is a nucleotide sequence
encoding the novel receptor of the present invention
designated as "hXR2".
30

Sequence ID No. 8 is the amino acid sequence
35 deduced from the nucleotide sequence set forth in Sequence

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ID No. 7 (variously referred to herein as receptor "XR2", "hXR2" or "hXR2.pep").

Sequence ID No. 9 is a nucleotide sequence
5 encoding novel receptor of the present invention referred
to herein as "mXR4".

Sequence ID No. 10 is the amino acid sequence
deduced from the nucleotide sequence of Sequence ID No. 9
10 (variously referred to herein as receptor "XR4", "mXR4" or
"mXR4.pep").

Sequence ID No. 11 is the nucleotide sequence
encoding the novel receptor of the present invention
15 referred to as "mXR5".

Sequence ID No. 12 is the amino acid sequence
deduced from the nucleotide sequence of Sequence ID No. 11
(variously referred to herein as receptor "XR5", "mXR5" or
20 "mXR5.pep").

Sequence ID No. 13 is the nucleotide sequence
encoding the novel receptor of the present invention
referred to as "dXR79".

25

Sequence ID No. 14 is the amino acid sequence
deduced from the nucleotide sequence of Sequence ID No. 13
(variously referred to herein as "XR79", "dXR79" or
"dXR79.pep").

30

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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BORGMEYER Ph.D., UWE K.
GIGUERE Ph.D., VINCENT NMN
YAO Mr., TSO-PANG NMN

(ii) TITLE OF INVENTION: NOVEL RECEPTORS

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: US
(F) ZIP: 90071-2921

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter Ph.D., Stephen E.
(B) REGISTRATION NUMBER: 31192
(C) REFERENCE/DOCKET NUMBER: P31 8936

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 535-9001
(B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1952 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: XR1 (VERHT19.SEQ)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 79..1725

(1x) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 349..1952

(D) OTHER INFORMATION: /product= "Carboxy terminal porti n
of Xr1 variant verht3"

(1x) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 352..1952

(D) OTHER INFORMATION: /product= "Carboxy terminal portion
of Xr1 variant verhr5"

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGGG ACTCCATAGT ACACTGGGGC AAAGCACAGC CCCAGTTTCT GGAGGCAGAT	60
GGGTAACCAG GAAAAGGC ATG AAT GAG GGG GCC CCA GGA GAC AGT GAC TTA	111
Met Asn Glu Gly Ala Pro Gly Asp Ser Asp Leu	
1 5 10	
GAG ACT GAG GCA AGA GTG CCG TGG TCA ATC ATG GGT CAT TGT CTT CGA	159
Glu Thr Glu Ala Arg Val Pro Trp Ser Ile Met Gly His Cys Leu Arg	
15 20 25	
ACT GGA CAG GCC AGA ATG TCT GCC ACA CCC AGA CCT GCA GGT GAA GGA	207
Thr Gly Gln Ala Arg Met Ser Ala Thr Pro Thr Pro Ala Gly Glu Gly	
30 35 40	
GCC AGA AGC TCT TCA ACC TGT AGC TCC CTG AGC AGG CTG TTC TGG TCT	255
Ala Arg Ser Ser Ser Thr Cys Ser Ser Leu Ser Arg Leu Phe Trp Ser	
45 50 55	
CAA CTT GAG CAC ATA AAC TGG GAT GGA GCC ACA GCC AAG AAC TTT ATT	303
Gln Leu Glu His Ile Asn Trp Asp Gly Ala Thr Ala Lys Asn Phe Ile	
60 65 70 75	
AAT TTA AGG GAG TTC TTC TCT TTT CTG CTC CCT GCA TTG AGA AAA GCT	351
Asn Leu Arg Glu Phe Phe Ser Phe Leu Leu Pro Ala Leu Arg Lys Ala	
80 85 90	
CAA ATT GAA ATT ATT CCA TGC AAG ATC TGT GGA GAC AAA TCA TCA GGA	399
Gln Ile Glu Ile Ile Pro Cys Lys Ile Cys Gly Asp Lys Ser Ser Gly	
95 100 105	
ATC CAT TAT GGT GTC ATT ACA TGT GAA GCC TGC AAG GCC TTT TTC AGG	447
Ile His Tyr Gly Val Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg	
110 115 120	
AGA AGT CAG CAA AGC AAT GCC ACC TAC TCC TGT CCT CGT CAG AAG AAC	495
Arg Ser Gln Gln Ser Asn Ala Thr Tyr Ser Cys Pro Arg Gln Lys Asn	
125 130 135	
TGT TTG ATT GAT CGA ACC AGT AGA AAC CGC TGC CAA CAC TGT CGA TTA	543
Cys Leu Ile Asp Arg Thr Ser Arg Asn Arg Cys Gln His Cys Arg Leu	
140 145 150 155	
CAG AAA TGC CTT GCC GTA GGG ATG TCT CGA GAT GCT GTA AAA TTT GGC	591
Gln Lys Cys Leu Ala Val Gly Met Ser Arg Asp Ala Val Lys Phe Gly	
160 165 170	
CGA ATG TCA AAA AAG CAG AGA GAC AGC TTG TAT GCA GAA GTA CAG AAA	639
Arg Met Ser Lys Lys Gln Arg Asp Ser Leu Tyr Ala Glu Val Gln Lys	
175 180 185	

CAC His	CGG Arg	ATG Met 190	CAG Gln	CAG Gln	CAG Gln	CAG Gln	CGC Arg 195	GAC Asp	CAC His	CAG Gln	CAG Gln	CAG Gln	CCT Pro 200	GGA Gly	GAG Glu	687
GCT Ala 205	GAG Glu	CCG Pro	CTG Leu	ACG Thr	CCC Pro	ACC Thr 210	TAC Tyr	AAC Asn	ATC Ile	TCG Ser	GCC Ala 215	AAC Asn	GGG Gly	CTG Leu	ACG Thr	735
GAA Glu 220	CTT Leu	CAC His	GAC Asp	GAC Asp	CTC Leu 225	AGT Ser	AAC Asn	TAC Tyr	ATT Ile	GAC Asp 230	GGG Gly	CAC His	ACC Thr	CCT Pro	GAG Glu 235	783
GGG Gly	AGT Ser	AAG Lys	GCA Ala	GAC Asp 240	TCC Ser	GCC Ala	GTC Val	AGC Ser	AGC Ser 245	TTC Phe	TAC Tyr	CTG Leu	GAC Asp	ATA Ile 250	CAG Gln	831
CCT Pro	TCC Ser	CCA Pro	GAC Asp 255	CAG Gln	TCA Ser	GGT Gly	CTT Leu	GAT Asp 260	ATC Ile	AAT Asn	GGA Gly	ATC Ile	AAA Lys 265	CCA Pro	GAA Glu	879
CCA Pro	ATA Ile	TGT Cys 270	GAC Asp	TAC Tyr	ACA Thr	CCA Pro	GCA Ala 275	TCA Ser	GGC Gly	TTC Phe	TTT Phe	CCC Pro 280	TAC Tyr	TGT Cys	TCG Ser	927
TTC Phe	ACC Thr 285	AAC Asn	GGC Gly	GAG Glu	ACT Thr	TCC Ser 290	CCA Pro	ACT Thr	GTG Val	TCC Ser 295	ATG Met	GCA Ala	GAA Glu	TTA Leu	GAA Glu	975
CAC His 300	CTT Leu	GCA Ala	CAG Gln	AAT Asn	ATA Ile 305	TCT Ser	AAA Lys	TCG Ser	CAT His	CTG Leu 310	GAA Glu	ACC Thr	TGC Cys	CAA Gln	TAC Tyr 315	1023
TTG Leu	AGA Arg	GAA Glu	GAG Glu	CTC Leu 320	CAG Gln	CAG Gln	ATA Ile	ACG Thr	TGG Trp 325	CAG Gln	ACC Thr	TTT Phe	TTA Leu	CAG Gln 330	GAA Glu	1071
GAA Glu	ATT Ile	GAG Glu	AAC Asn 335	TAT Tyr	CAA Gln	AAC Asn	AAG Lys	CAG Gln 340	CGG Arg	GAG Glu	GTG Val	ATG Met	TGG Trp 345	CAA Gln	TTG Leu	1119
TGT Cys	GCC Ala	ATC Ile 350	AAA Lys	ATT Ile	ACA Thr	GAA Glu	GCT Ala 355	ATA Ile	CAG Gln	TAT Tyr	GTG Val	GTG Val 360	GAG Glu	TTT Phe	GCC Ala	1167
AAA Lys	CGC Arg 365	ATT Ile	GAT Asp	GGA Gly	TTT Phe	ATG Met 370	GAA Glu	GTG Leu	TGT Cys	CAA Gln	AAT Asn 375	GAT Asp	CAA Gln	ATT Ile	GTG Val	1215
CTT Leu 380	CTA Leu	AAA Lys	GCA Ala	GGT Gly	TCT Ser 385	CTA Leu	GAG Glu	GTG Val	GTG Val	TTT Phe 390	ATC Ile	AGA Arg	ATG Met	TGC Cys	CGT Arg 395	1263
GCC Ala	TTT Phe	GAC Asp	TCT Ser	CAG Gln 400	AAC Asn	AAC Asn	ACC Thr	GTG Val 405	TAC Tyr	TTT Phe	GAT Asp	GGG Gly	AAG Lys	TAT Tyr 410	GCC Ala	1311
AGC Ser	CCC Pro	GAC Asp 415	GTG Val	TTC Phe	AAA Lys	TCC Ser	TTA Leu	GGT Gly 420	TGT Cys	GAA Glu	GAC Asp	TTT Phe	ATT Ile 425	AGC Ser	TTT Phe	1359
GTG Val	TTT Phe	GAA Glu 430	TTT Phe	GCA Gly	AAG Lys	AGT Ser	TTA Leu 435	TGT Cys	TCT Ser	ATG Met	CAC His	CTG Leu 440	ACT Thr	GAA Glu	GAT Asp	1407
GAA Glu 445	ATT Ile	GCA Ala	TTA Leu	TTT Phe	TCT Ser	GCA Ala 450	TTT Phe	GTA Val	CTG Leu	ATG Met	TCA Ser 455	GCA Ala	GAT Asp	CGC Arg	TCA Ser	1455

TGG CTG CAA GAA AAG GTA AAA ATT GAA AAA CTG CAA CAG AAA ATT CAG 1503
 Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys Ile Gln
 460 465 470 475

CTA GCT CTT CAA CAC GTC CTA CAG AAG AAT CAC CGA GAA GAT CGA ATA 1551
 Leu Ala Leu Gln His Val Leu Gln Lys Asn His Arg Glu Asp Gly Ile
 480 485 490

CTA ACA AAG TTA ATA TGC AAG GTG TCT ACA TTA AGA GCC TTA TGT GGA 1599
 Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu Cys Gly
 495 500 505

CGA CAT ACA GAA AAG CTA ATG GCA TTT AAA GCA ATA TAC CCA GAC ATT 1647
 Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro Asp Ile
 510 515 520

GTG CGA CTT CAT TTT CCT CCA TTA TAC AAG GAG TTG TTC ACT TCA GAA 1695
 Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr Ser Glu
 525 530 535

TTT GAG CCA GCA ATG CAA ATT GAT GGG TAAATGTTAT CACCTAAGCA 1742
 Phe Glu Pro Ala Met Gln Ile Asp Gly
 540 545

CTTCTAGAAT GTCTGAAGTA CAAACATGAA AAACAAACAA AAAAAATTAAC CGAGACACTT 1802

TATATGGCCC TGCAGAGACC TGGAGCGCCA CACACTGCAC ATCTTTTGGT GATCGGGGTC 1862

AGGCAAAGGA GGGGAAACAA TGA AAACAAA TAAAGTTGAA CTTGTTTTTC TCAAAAAAAA 1922

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1952

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Glu Gly Ala Pro Gly Asp Ser Asp Leu Glu Thr Glu Ala Arg
 1 5 10 15
 Val Pro Trp Ser Ile Met Gly His Cys Leu Arg Thr Gly Gln Ala Arg
 20 25 30
 Met Ser Ala Thr Pro Thr Pro Ala Gly Glu Gly Ala Arg Ser Ser Ser
 35 40 45
 Thr Cys Ser Ser Leu Ser Arg Leu Phe Trp Ser Gln Leu Glu His Ile
 50 55 60
 Asn Trp Asp Gly Ala Thr Ala Lys Asn Phe Ile Asn Leu Arg Glu Phe
 65 70 75 80
 Phe Ser Phe Leu Leu Pro Ala Leu Arg Lys Ala Gln Ile Glu Ile Ile
 85 90 95
 Pro Cys Lys Ile Cys Gly Asp Lys Ser Ser Gly Ile His Tyr Gly Val
 100 105 110
 Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Gln Ser
 115 120 125

Asn Ala Thr Tyr Ser Cys Pr Arg Gln Lys Asn Cys Leu Ile Asp Arg
 130 135 140
 Thr Ser Arg Asn Arg Cys Gln His Cys Arg Leu Gln Lys Cys Leu Ala
 145 150 155 160
~~Val Gly Met S r Arg Asp Ala Val Lys Ph Gly Arg Met Ser Lys Lys~~
~~165 170 175~~
 Gln Arg Asp Ser Leu Tyr Ala Glu Val Gln Lys His Arg Met Gln Gln
 180 185 190
 Gln Gln Arg Asp His Gln Gln Gln Pro Gly Glu Ala Glu Pro Leu Thr
 195 200 205
 Pro Thr Tyr Asn Ile Ser Ala Asn Gly Leu Thr Glu Leu His Asp Asp
 210 215 220
 Leu Ser Asn Tyr Ile Asp Gly His Thr Pro Glu Gly Ser Lys Ala Asp
 225 230 235 240
 Ser Ala Val Ser Ser Phe Tyr Leu Asp Ile Gln Pro Ser Pro Asp Gln
 245 250 255
 Ser Gly Leu Asp Ile Asn Gly Ile Lys Pro Glu Pro Ile Cys Asp Tyr
 260 265 270
 Thr Pro Ala Ser Gly Phe Phe Pro Tyr Cys Ser Phe Thr Asn Gly Glu
 275 280 285
 Thr Ser Pro Thr Val Ser Met Ala Glu Leu Glu His Leu Ala Gln Asn
 290 295 300
 Ile Ser Lys Ser His Leu Glu Thr Cys Gln Tyr Leu Arg Glu Glu Leu
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 Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Ile Asp Gly
 355 360 365
 Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Val Leu Leu Lys Ala Gly
 370 375 380
 Ser Leu Glu Val Val Phe Ile Arg Met Cys Arg Ala Phe Asp Ser Gln
 385 390 395 400
 Asn Asn Thr Val Tyr Phe Asp Gly Lys Tyr Ala Ser Pro Asp Val Phe
 405 410 415
 Lys Ser Leu Gly Cys Glu Asp Phe Ile Ser Phe Val Phe Glu Phe Gly
 420 425 430
 Lys Ser Leu Cys Ser Met His Leu Thr Glu Asp Glu Ile Ala Leu Phe
 435 440 445
 Ser Ala Phe Val Leu Met Ser Ala Asp Arg Ser Trp Leu Gln Glu Lys
 450 455 460
 Val Lys Ile Glu Lys Leu Gln Gln Lys Ile Gln Leu Ala Leu Gln His
 465 470 475 480

Val Leu Gln Lys Asn His Arg Glu Asp Gly Ile Leu Thr Lys Leu Ile
 485 490 495

Cys Lys Val Ser Thr Leu Arg Ala Leu Cys Gly Arg His Thr Glu Lys
 500 505 510

Leu Met Ala Phe Lys Ala Ile Tyr Pro Asp Ile Val Arg Leu His Phe
 515 520 525

Pro Pro Leu Tyr Lys Glu Leu Phe Thr Ser Glu Phe Glu Pro Ala Met
 530 535 540

Gln Ile Asp Gly
 545

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: AMINO TERMINAL PORTION OF XR1PRIME (VERHT3.SEQ)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 90..386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATCTGTCT GATCACCTTG GACTCCATAG TACACTGGGG CAAAGCACAG CCCAGTTTC	60
TGGAGGCAGA TCGGTAACCA GGAAAAGGC ATG AAT GAG GGG GCC CCA GGA GAC	113
Met Asn Glu Gly Ala Pro Gly Asp	
1 5	
AGT GAC TTA GAG ACT GAG GCA AGA GTG CCG TGG TCA ATC ATG GGT CAT	161
Ser Asp Leu Glu Thr Glu Ala Arg Val Pro Trp Ser Ile Met Gly His	
10 15 20	
TGT CTT CGA ACT GGA CAG GCC AGA ATG TCT GCC ACA CCC ACA CCT GCA	209
Cys Leu Arg Thr Gly Gln Ala Arg Met Ser Ala Thr Pro Thr Pro Ala	
25 30 35 40	
GGT GAA GGA GCC AGA AGG GAT GAA CTT TTT GGG ATT CTC CAA ATA CTC	257
Gly Glu Gly Ala Arg Arg Asp Glu Leu Phe Gly Ile Leu Gln Ile Leu	
45 50 55	
CAT CAG TGT ATC CTG TCT TCA GGT GAT GCT TTT GTT CTT ACT GGC GTC	305
His Gln Cys Ile Leu Ser Ser Gly Asp Ala Phe Val Leu Thr Gly Val	
60 65 70	
TGT TGT TCC TCG AGG CAG AAT GGC AAG CCA CCA TAT TCA CAA AAG GAA	353
Cys Cys Ser Trp Arg Gln Asn Gly Lys Pro Pro Tyr Ser Gln Lys Glu	
75 80 85	
GAT AAG GAA GTA CAA ACT GGA TAC ATG AAT GCT	386
Asp Lys Glu Val Gln Thr Gly Tyr Met Asn Ala	
90 95	

(2) INFORMATION FOR SEQ ID NO:4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Asn Glu Gly Ala Pro Gly Asp Ser Asp Leu Glu Thr Glu Ala Arg
 1           5           10           15
Val Pro Trp Ser Ile Met Gly His Cys Leu Arg Thr Gly Gln Ala Arg
          20           25           30
Met Ser Ala Thr Pro Thr Pro Ala Gly Glu Gly Ala Arg Arg Asp Glu
          35           40           45
Leu Phe Gly Ile Leu Gln Ile Leu His Gln Cys Ile Leu Ser Ser Gly
 50           55           60
Asp Ala Phe Val Leu Thr Gly Val Cys Cys Ser Trp Arg Gln Asn Gly
 65           70           75           80
Lys Pro Pro Tyr Ser Gln Lys Glu Asp Lys Glu Val Gln Thr Gly Tyr
          85           90           95
Met Asn Ala

```

(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: AMINO TERMINAL PORTION OF XR1PRIM2 (VERHR5.SEQ)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 103..300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GTTTTTTTTT TTTTITGCT ACCATAGAGT TGCTCTGAAA ACAGAAGATA GAGGGAGTCT      60
CGGAGCTCGC CATCTCCAGC GATCTCTACA TTGGGAAAAA AC ATG GAG TCA GCT      114
                                     Met Glu Ser Ala
                                     1
CCG GCA AGG GAG ACC CCG CTG AAC CAG GAA TCC GCC GCC CCC GAC CCC      162
Pro Ala Arg Glu Thr Pro Leu Asn Gln Glu Ser Ala Ala Pro Asp Pro
 5           10           15           20
GCC GCC AGC GAG CCA GGC AGC AGC GGC GCG GAC GCG GCC GCC GGC TCC      210
Ala Ala Ser Glu Pro Gly Ser Ser Gly Ala Asp Ala Ala Ala Gly Ser
          25           30           35

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CGC AAG AGC GAG CCG CCT GCC CCG GTG CGC AGA CAG AGC TAT TCC AGC	258
Arg Lys Ser Glu Pro Pro Ala Pro Val Arg Arg Gln Ser Tyr Ser Ser	
40 45 50	
ACC AGC AGA GGT ATC TCA GTA ACG AAG AAG ACA CAT ACA TCT	300
Thr Ser Arg Gly Ile Ser Val Thr Lys Lys Thr His Thr Ser	
55 60 65	

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Ser Ala Pro Ala Arg Glu Thr Pro Leu Asn Gln Glu Ser Ala	
1 5 10 15	
Ala Pro Asp Pro Ala Ala Ser Glu Pro Gly Ser Ser Gly Ala Asp Ala	
20 25 30	
Ala Ala Gly Ser Arg Lys Ser Glu Pro Pro Ala Pro Val Arg Arg Gln	
35 40 45	
Ser Tyr Ser Ser Thr Ser Arg Gly Ile Ser Val Thr Lys Lys Thr His	
50 55 60	
Thr Ser	
65	

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: XR2 (XR2.SEG)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 148..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATATCCGTG ACATCATTCG CTGAGTCCAC TGCAAAAAGC TGTCCCCAGA GCAGGAGGGC	60
AATGACAGCT CCCAGGGCAC TCATCTTGAC TGCTCTTGCC TGGGGATTTC GACAGTGCCT	120
TGTAATGAC CAGGGCTCCA GAAAGAG ATG TCC TTG TGG CTG GGG GCC CCT	171
Met Ser Leu Trp Leu Gly Ala Pr	
1 5	
GTG CCT GAC ATT CCT CCT GAC TCT GCG GTG GAG CTG TGG AAG CCA GGC	219
Val Pro Asp Ile Pro Pro Asp Ser Ala Val Glu Leu Trp Lys Pro Gly	
10 15 20	

GCA CAG GAT GCA AGC AGC CAG GCC CAG GGA GGC AGC AGC TGC ATC CTC Ala Gln Asp Ala Ser S r Gln Ala Gln Gly Gly Ser Ser Cys Il Leu 25 30 35 40	267
AGA GAG GAA GCC AGG ATG CCC CAC TCT GCT GGG GGT ACT GCA GAG CCC Arg Glu Glu Ala Arg Met Pro His Ser Ala Gly Gly Thr Ala Glu Pro 45 50 55	315
ACA GCC CTG CTC ACC AGG GCA GAG CCC CCT TCA GAA CCC ACA GAG ATC Thr Ala Leu Leu Thr Arg Ala Glu Pro Pro Ser Glu Pro Thr Glu Ile 60 65 70	363
CGT CCA CAA AAG CGG AAA AAG GGG CCA GCC CCC AAA ATG CTG GCG AAC Arg Pro Gln Lys Arg Lys Lys Gly Pro Ala Pro Lys Met Leu Gly Asn 75 80 85	411
GAG CTA TGC AGC GTG TGT GGG GAC AAG GCC TCG GGC TTC CAC TAC AAT Glu Leu Cys Ser Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn 90 95 100	459
GTT CTG AGC TGC GAG GGC TGC AAG GCA TTC TTC CGC CGC AGC GTC ATC Val Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Ile 105 110 115 120	507
AAG GGA GCG CAC TAC ATC TGC CAC AGT GGC GGC CAC TGC CCC ATG GAC Lys Gly Ala His Tyr Ile Cys His Ser Gly Gly His Cys Pro Met Asp 125 130 135	555
ACC TAC ATG CGT CGC AAG TGC CAG GAG TGT CGG CTT CGC AAA TGC CGT Thr Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Arg 140 145 150	603
CAG GCT GGC ATG CGG GAG GAG TGT GTC CTG TCA GAA GAA CAG ATC CGC Gln Ala Gly Met Arg Glu Glu Cys Val Leu Ser Glu Glu Gln Ile Arg 155 160 165	651
CTG AAG AAA CTG AAG CGG CAA GAG GAG GAA CAG GCT CAT GCC ACA TCC Leu Lys Lys Leu Lys Arg Gln Glu Glu Glu Gln Ala His Ala Thr Ser 170 175 180	699
TTG CCC CCC AGG CGT TCC TCA CCC CCC CAA ATC CTG CCC CAG CTC AGC Leu Pro Pro Arg Arg Ser Ser Pro Pro Gln Ile Leu Pro Gln Leu Ser 185 190 195 200	747
CCG GAA CAA CTG GGC ATG ATC GAG AAG CTC GTC GCT GCC CAG CAA CAG Pro Glu Gln Leu Gly Met Ile Glu Lys Leu Val Ala Ala Gln Gln Gln 205 210 215	795
TGT AAC CGG CGC TCC TTT TCT GAC CGG CTT CGA GTC ACG CCT TGG CCC Cys Asn Arg Arg Ser Phe Ser Asp Arg Leu Arg Val Thr Pro Trp Pro 220 225 230	843
ATG GCA CCA GAT CCC CAT AGC CGG GAG GCC CGT CAG CAG CGC TTT GCC Met Ala Pro Asp Pro His Ser Arg Glu Ala Arg Gln Gln Arg Phe Ala 235 240 245	891
CAC TTC ACT GAG CTG GCC ATC GTC TCT GTG CAG GAG ATA GTT GAC TTT His Phe Thr Glu Leu Ala Ile Val Ser Val Gln Glu Ile Val Asp Phe 250 255 260	939
GCT AAA CAG CTA CCC GGC TTC CTG CAG CTC AGC CGG GAG GAC CAG ATT Ala Lys Gln Leu Pro Gly Phe Leu Gln Leu Ser Arg Glu Asp Gln Ile 265 270 275 280	987
GCC CTG CTG AAG ACC TCT GCG ATC GAG GTG ATG CTT CTG CAG ACA TCT Ala Leu Leu Lys Thr Ser Ala Ile Glu Val Met Leu Leu Glu Thr Ser 285 290 295	1035

CCG AGG TAC AAC CCT GGG AGT GAG AGT ATC ACC TTC CTC AAG GAT TTC Arg Arg Tyr Asn Pro Gly Ser Glu Ser Ile Thr Phe Leu Lys Asp Phe 300 305 310	1083
AGT TAT AAC CGG GAA GAC TTT GCC AAA GCA GCG CTG CAA GTG GAA TTC Ser Tyr Asn Arg Glu Asp Phe Ala Lys Ala Gly Leu Gln Val Glu Phe 315 320 325	1131
ATC AAC CCC ATC TTC GAG TTC TCC AGG GCC ATG AAT GAG CTG CAA CTC Ile Asn Pro Ile Phe Glu Phe Ser Arg Ala Met Asn Glu Leu Gln Leu 330 335 340	1179
AAT GAT GCC GAG TTT GCC TTG CTC ATT GCT ATC AGC ATC TTC TCT GCA Asn Asp Ala Glu Phe Ala Leu Leu Ile Ala Ile Ser Ile Phe Ser Ala 345 350 355 360	1227
GAC CGG CCC AAC GTG CAG GAC CAG CTC CAG GTG GAG AGG CTG CAG CAC Asp Arg Pro Asn Val Gln Asp Gln Leu Gln Val Glu Arg Leu Gln His 365 370 375	1275
ACA TAT GTG GAA GCC CTG CAT GCC TAC GTC TCC ATC CAC CAT CCC CAT Thr Tyr Val Glu Ala Leu His Ala Tyr Val Ser Ile His His Pro His 380 385 390	1323
GAC CGA CTG ATG TTC CCA CGG ATG CTA ATG AAA CTG GTG AGC CTC CGG Asp Arg Leu Met Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg 395 400 405	1371
ACC CTG AGC AGC GTC CAC TCA GAG CAA GTG TTT GCA CTG CGT CTG CAG Thr Leu Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln 410 415 420	1419
GAC AAA AAG CTC CCA CCG CTG CTC TCT GAG ATC TGG GAT GTG CAC GAA Asp Lys Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu 425 430 435 440	1467
TGACTGTTCT GTCCCATAT TTTCTGTTT CTGGCCCGGA TGGCTGAGGC CTGGTGGCTG	1527
CCTCCTAGAA GTGGAACAGA CTGAGAAGGG CAAACATTCC TGGGAGCTGG GCAAGGAGAT	1587
CCTCCCGTGG CATTAAAAGA GAGTCAAAGC GTAAAAA AAAA AAAAAA AAAAAA	1647
AAAAAGGAAT TC	1659

(2) INFORMATION FOR SEQ ID NO:8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Leu Trp Leu Gly Ala Pro Val Pro Asp Ile Pro Pro Asp Ser
1 5 10 15

Ala Val Glu Leu Trp Lys Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala
20 25 30

Gln Gly Gly Ser Ser Cys Ile Leu Arg Glu Glu Ala Arg Met Pro His
35 40 45

Ser Ala Gly Gly Thr Ala Glu Pro Thr Ala Leu Leu Thr Arg Ala Glu
50 55 60

Pro 65 Pro S r Glu 70 Pro Thr Glu 75 Ile Arg Pr Gln Lys Arg Lys Lys Gly 80
 Pro Ala Pro Lys Met 85 Leu Gly Asn Glu 90 Leu Cys Ser Val Cys Gly Asp 95
 Lys Ala Ser Gly 100 Phe His Tyr Asn Val 105 Leu Ser Cys Glu Gly Cys Lys 110
 Gly Phe Phe Arg Arg Ser Val Ile Lys Gly Ala His Tyr Ile Cys His 115 120 125
 Ser Gly Gly His Cys Pro Met Asp Thr Tyr Met Arg Arg Lys Cys Gln 130 135 140
 Glu Cys Arg Leu Arg Lys Cys Arg Gln Ala Gly Met Arg Glu Glu Cys 145 150 155 160
 Val Leu Ser Glu Glu Gln Ile Arg Leu Lys Lys Leu Lys Arg Gln Glu 165 170 175
 Glu Glu Gln Ala His Ala Thr Ser Leu Pro Pro Arg Arg Ser Ser Pro 180 185 190
 Pro Gln Ile Leu Pro Gln Leu Ser Pro Glu Gln Leu Gly Met Ile Glu 195 200 205
 Lys Leu Val Ala Ala Gln Gln Gln Cys Asn Arg Arg Ser Phe Ser Asp 210 215 220
 Arg Leu Arg Val Thr Pro Trp Pro Met Ala Pro Asp Pro His Ser Arg 225 230 235 240
 Glu Ala Arg Gln Gln Arg Phe Ala His Phe Thr Glu Leu Ala Ile Val 245 250 255
 Ser Val Gln Glu Ile Val Asp Phe Ala Lys Gln Leu Pro Gly Phe Leu 260 265 270
 Gln Leu Ser Arg Glu Asp Gln Ile Ala Leu Leu Lys Thr Ser Ala Ile 275 280 285
 Glu Val Met Leu Leu Glu Thr Ser Arg Arg Tyr Asn Pro Gly Ser Glu 290 295 300
 Ser Ile Thr Phe Leu Lys Asp Phe Ser Tyr Asn Arg Glu Asp Phe Ala 305 310 315 320
 Lys Ala Gly Leu Gln Val Glu Phe Ile Asn Pro Ile Phe Glu Phe Ser 325 330 335
 Arg Ala Met Asn Glu Leu Gln Leu Asn Asp Ala Glu Phe Ala Leu Leu 340 345 350
 Ile Ala Ile Ser Ile Phe Ser Ala Asp Arg Pro Asn Val Gln Asp Gln 355 360 365
 Leu Gln Val Glu Arg Leu Gln His Thr Tyr Val Glu Ala Leu His Ala 370 375 380
 Tyr Val Ser Ile His His Pr His Asp Arg Leu Met Phe Pr Arg Met 385 390 395 400
 Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser Val His Ser Glu 405 410 415

Gln Val Phe Ala Leu Arg Leu Gln Asp Lys Lys Leu Pr Pro Leu Leu
 420 425 430
 Ser Glu Ile Trp Asp Val His Glu
 435 440

(2) INFORMATION FOR SEQ ID NO:9:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2009 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(v11) IMMEDIATE SOURCE:
 (B) CLONE: XR4 (XR4.SEG)

(1x) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 263..1582

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCCTG GGGATTAAATG CGAAAAGTTT TGGCAGGAGC TGGGGGATTC TCGGGAGCCT	60
GCGGGACGGC GGCAGCGGCG CGAGAGGCGG CCGGCACACT GCTGTGCAGC GGTGTGGGTA	120
TGCGCATGGG ACTCACTCAG AGGCTCCTGC TCACTGACAG ATGAAGACAA ACCCACGGTA	180
AAGGCAGTCC ATCTGCGCTC AGACCCAGAT GGTGGCAGAG CTATGACCAG GCCTGCAGCG	240
CCACGCCAAG TGGGGGTCAG TC ATG GAA CAG CCA CAG GAG GAG ACC CCT GAG	292
Met Glu Gln Pro Gln Glu Glu Thr Pro Glu	10
1 5	
GCC CGG GAA GAG GAG AAA GAG GAA GTG GCC ATG GGT CAC GGA GCC CCG	340
Ala Arg Glu Glu Glu Lys Glu Glu Val Ala Met Gly Asp Gly Ala Pro	25
15 20	
GAG CTC AAT GGG GCA CCA GAA CAC ACG CTT CCT TCC AGC AGC TGT GCA	388
Glu Leu Asn Gly Gly Pro Glu His Thr Leu Pro Ser Ser Ser Cys Ala	40
30 35	
GAC CTC TCC CAG AAT TCC TCC CCT TCC TCC CTG CTG GAC CAG CTG CAG	436
Asp Leu Ser Gln Asn Ser Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln	55
45 50	
ATG GGC TGT GAT GGG GCC TCA GGC GGC AGC CTC AAC ATG GAA TGT CCG	484
Met Gly Cys Asp Gly Ala Ser Gly Gly Ser Leu Asn Met Glu Cys Arg	70
60 65	
GTG TGC GGG GAC AAG GCC TCG GGC TTC CAC TAC GGG GTC CAC GCG TGC	532
Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys	90
75 80 85	
GAG GGC TGC AAG GGC TTC TTC CGC CGG ACA ATC CGC ATG AAG CTC GAG	580
Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu	105
95 100	

TAT	GAG	AAG	TGC	GAT	CGG	ATC	TGC	AAG	ATC	CAG	AAG	AAG	AAC	CGC	AAC	628
Tyr	Glu	Lys	Cys	Asp	Arg	Ile	Cys	Lys	Ile	Gln	Lys	Lys	Asn	Arg	Asn	
			110					115					120			
AAG	TGT	CAG	TAC	TGC	CGC	TTC	CAG	AAG	TGC	CTG	GCA	CTC	GGC	ATG	TCG	676
Lys	Cys	Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Leu	Gly	Met	Ser	
		125					130					135				
CAC	AAC	GCT	ATC	CGC	TTT	GGA	CGG	ATG	CCG	GAC	GGC	GAG	AAG	AGG	AAG	724
His	Asn	Ala	Ile	Arg	Phe	Gly	Arg	Met	Pro	Asp	Gly	Glu	Lys	Arg	Lys	
	140					145					150					
CTG	GTG	GCG	GGG	CTG	ACT	GCC	AGC	GAG	GGG	TGC	CAG	CAC	AAC	CCC	CAG	772
Leu	Val	Ala	Gly	Leu	Thr	Ala	Ser	Glu	Gly	Cys	Gln	His	Asn	Pro	Gln	
155					160					165					170	
CTG	GCC	GAC	CTG	AAG	GCC	TTC	TCT	AAG	CAC	ATC	TAC	AAC	GCC	TAC	CTG	820
Leu	Ala	Asp	Leu	Lys	Ala	Phe	Ser	Lys	His	Ile	Tyr	Asn	Ala	Tyr	Leu	
				175					180					185		
AAA	AAC	TTC	AAC	ATG	ACC	AAA	AAG	AAG	GCC	CGG	AGC	ATC	CTC	ACC	GGC	868
Lys	Asn	Phe	Asn	Met	Thr	Lys	Lys	Lys	Ala	Arg	Ser	Ile	Leu	Thr	Gly	
			190					195					200			
AAG	TCC	AGC	CAC	AAC	GCA	CCC	TTT	GTG	ATC	CAC	GAC	ATC	GAG	ACA	CTG	916
Lys	Ser	Ser	His	Asn	Ala	Pro	Phe	Val	Ile	His	Asp	Ile	Glu	Thr	Leu	
		205				210						215				
TGG	CAG	GCA	GAG	AAG	GGC	CTG	GTG	TGG	AAA	CAG	CTG	GTG	AAC	GTG	CCG	964
Trp	Gln	Ala	Glu	Lys	Gly	Leu	Val	Trp	Lys	Gln	Leu	Val	Asn	Val	Pro	
	220					225					230					
CCC	TAC	AAC	GAG	ATC	AGT	GTG	CAC	GTG	TTC	TAC	CGC	TGC	CAG	TCC	ACC	1012
Pro	Tyr	Asn	Glu	Ile	Ser	Val	His	Val	Phe	Tyr	Arg	Cys	Gln	Ser	Thr	
235					240					245					250	
ACA	GTG	GAG	ACA	GTG	CGA	GAG	CTC	ACC	GAG	TTC	GCC	AAG	AAC	ATC	CCC	1060
Thr	Val	Glu	Thr	Val	Arg	Glu	Leu	Thr	Glu	Phe	Ala	Lys	Asn	Ile	Pro	
				255					260					265		
AAC	TTC	AGC	AGC	CTC	TTC	CTC	AAT	GAC	CAG	GTG	ACC	CTC	CTC	AAG	TAT	1108
Asn	Phe	Ser	Ser	Leu	Phe	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	
			270					275					280			
GGC	GTG	CAC	GAG	GCC	ATC	TTT	GCC	ATG	CTG	GCC	TCC	ATC	GTG	AAC	AAA	1156
Gly	Val	His	Glu	Ala	Ile	Phe	Ala	Met	Leu	Ala	Ser	Ile	Val	Asn	Lys	
		285				290						295				
GAC	GGG	CTG	CTG	GTG	GCC	AAC	GGC	AGT	GGC	TTC	GTG	ACC	CAC	GAG	TTC	1204
Asp	Gly	Leu	Leu	Val	Ala	Asn	Gly	Ser	Gly	Phe	Val	Thr	His	Glu	Phe	
	300					305					310					
TTG	CGA	AGT	CTC	CGC	AAG	CCC	TTC	AGT	GAC	ATC	ATT	GAG	CCC	AAG	TTC	1252
Leu	Arg	Ser	Leu	Arg	Lys	Pro	Phe	Ser	Asp	Ile	Ile	Glu	Pro	Lys	Phe	
315					320					325					330	
GAG	TTT	GCT	GTG	AAG	TTC	AAT	GCG	CTG	GAG	CTC	GAT	GAC	AGT	GAC	CTG	1300
Glu	Phe	Ala	Val	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	
				335					340					345		
GCG	CTC	TTC	ATC	GCG	GCC	ATC	ATT	CTG	TGT	GGA	GAC	CGG	CCA	CGC	CTC	1348
Ala	Leu	Ph	Ile	Ala	Ala	Ile	Ile	Leu	Cys	Gly	Asp	Arg	Pro	Gly	Leu	
			350					355					360			
ATG	AAT	GTG	CCC	CAG	GTA	GAA	GCC	ATC	CAG	GAC	ACC	ATT	CTG	CGG	GCT	1396
Met	Asn	Val	Pr	Gln	Val	Glu	Ala	Ile	Gln	Asp	Thr	Ile	Leu	Arg	Ala	
		365					370					375				

CTA GAA TTC CAT CTG CAG GTC AAC CAG CCT GAC AGC CAG TAC CTC TTC Leu Glu Phe His Leu Gln Val Asn His Pr Asp Ser Gln Tyr Leu Phe 380 385 390	1444
CCC AAG CTG CTG CAG AAG ATG GCA GAC CTG CGG CAC GTG GTC ACT GAG Pro Lys Leu Leu Gln Lys Met Ala Asp Leu Arg His Val Val Thr Glu 395 400 405 410	1492
CAT GCC CAG ATG ATG CAG TGG CTA AAG AAG ACG GAG AGT GAG ACC TTG His Ala Gln Met Met Gln Trp Leu Lys Lys Thr Glu Ser Glu Thr Leu 415 420 425	1540
CTG CAC CCC CTG CTC CAG GAA ATC TAC AAG GAC ATG TAC TAAGGCCGCA Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Met Tyr 430 435 440	1589
GCCCAGGCCT CCCCTCAGGC TCTGCTGGGC CCAGCCACGG ACTGTTGAGA GGACCAGCCA	1649
CAGGCACTGG CAGTCAAGCA GCTAGAGCCT ACTCACAACA CTCCAGACAC GTGCCCCAGA	1709
CTCTTCCCCC AACACGCCCA CCCCCACCAA CCCCCCATT CCCCCAACCC CCCTCCCCCA	1769
CCCCGCTCTC CCCATGGCCC GTTTCCTGTT TCTCCTCAGC ACCTCCTGTT CTTGCTGTCT	1829
CCCTAGCGCC CTTGCTCCCC CCCCTTTGCC TTCCTTCTCT AGCATCCCC TCGTCCAGT	1889
CCTCACATTT GTCTGATTCA CAGCAGACAG CCCGTGGTA CGCTCACCAG CAGCCTAAAA	1949
GCAGTGGGCC TGTGCTGGCC CAGTCCTGCC TCTCCTCTCT ATCCCCTTCA AAGGGAATTC	2009

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Glu	Gln	Pro	Gln	Glu	Glu	Thr	Pro	Glu	Ala	Arg	Glu	Glu	Glu	Lys	1	5	10	15
Glu	Glu	Val	Ala	Met	Gly	Asp	Gly	Ala	Pro	Glu	Leu	Asn	Gly	Gly	Pro	20	25	30	
Glu	His	Thr	Leu	Pro	Ser	Ser	Ser	Cys	Ala	Asp	Leu	Ser	Gln	Asn	Ser	35	40	45	
Ser	Pro	Ser	Ser	Leu	Leu	Asp	Gln	Leu	Gln	Met	Gly	Cys	Asp	Gly	Ala	50	55	60	
Ser	Gly	Gly	Ser	Leu	Asn	Met	Glu	Cys	Arg	Val	Cys	Gly	Asp	Lys	Ala	65	70	75	80
Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	Lys	Gly	Phe	85	90	95	
Phe	Arg	Arg	Thr	Ile	Arg	Met	Lys	Leu	Glu	Tyr	Glu	Lys	Cys	Asp	Arg	100	105	110	
Ile	Cys	Lys	Ile	Gln	Lys	Lys	Asn	Arg	Asn	Lys	Cys	Gln	Tyr	Cys	Arg	115	120	125	

Ph Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe
 130 135 140
 Gly Arg Met Pro Asp Gly Glu Lys Arg Lys Leu Val Ala Gly Leu Thr
 145 150 155 160
 Ala S r Glu Gly Cys Gln His Asn Pro Gln Leu Ala Asp Leu Lys Ala
 165 170 175
 Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr
 180 185 190
 Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala
 195 200 205
 Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly
 210 215 220
 Leu Val Trp Lys Gln Leu Val Asn Val Pro Pro Tyr Asn Glu Ile Ser
 225 230 235 240
 Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val Arg
 245 250 255
 Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu Phe
 260 265 270
 Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala Ile
 275 280 285
 Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val Ala
 290 295 300
 Asn Gly Ser Gly Phe Val Thr His Glu Phe Leu Arg Ser Leu Arg Lys
 305 310 315 320
 Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys Phe
 325 330 335
 Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala Ala
 340 345 350
 Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro Gln Val
 355 360 365
 Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu Gln
 370 375 380
 Val Asn His Pro Asp Ser Gln Tyr Leu Phe Pro Lys Leu Leu Gln Lys
 385 390 395 400
 Met Ala Asp Leu Arg His Val Val Thr Glu His Ala Gln Met Met Gln
 405 410 415
 Trp Leu Lys Lys Thr Glu Ser Glu Thr Leu Leu His Pro Leu Leu Gln
 420 425 430
 Glu Ile Tyr Lys Asp Met Tyr
 435

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: XR5 (XR5.SEG)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAA TTC CGC CGC GGA GCG GCG CGG CGC GAG GGG CCG GAG CCG GGC GGC	48
Glu Phe Arg Arg Gly Gly Ala Arg Arg Glu Gly Pro Glu Pro Gly Gly	
1 5 10 15	
TCA GGG GCC CAG AGA GTG CCG CCG CCG AGA GCC TGC CCG CCC CTG ACA	96
Ser Gly Ala Gln Arg Val Arg Arg Pro Arg Ala Cys Arg Pro Leu Thr	
20 25 30	
GCC CCC TCC CCC CGT GGA AGA CCA GGA CGA CGA CTA CGA AGG CGC AAG	144
Ala Pro Ser Pro Arg Gly Arg Pro Gly Arg Arg Leu Arg Arg Arg Lys	
35 40 45	
TCA TGG CCG AGC AGC GAA CGC CGA GAG GGC CCT GAG CAC CGC CGC ATG	192
Ser Trp Arg Ser Ser Glu Arg Arg Glu Gly Pro Glu His Arg Arg Met	
50 55 60	
GAG CGG GAC GAA CGG CCA CCT AGC GGA GCG GGA GGC GGC GGC GGC TCG	240
Glu Arg Asp Glu Arg Pro Pro Ser Gly Gly Gly Gly Gly Gly Ser	
65 70 75 80	
CGC GGG TTC CTG GAG CCG CCC GCC GCG CTC CCT CCG CCG CCG CCG AAC	288
Ala Gly Phe Leu Glu Pro Pro Ala Ala Leu Pro Pro Pro Pro Arg Asn	
85 90 95	
GGT TTC TGT CAG GAT GAA TTG GCA GAG CTT GAT CCA GGC ACT AAT GGA	336
Gly Phe Cys Gln Asp Glu Leu Ala Glu Leu Asp Pro Gly Thr Asn Gly	
100 105 110	
GAG ACT GAC AGT TTA ACA CTT GGC CAA GGC CAT ATA CCT GTT TCC GTC	384
Glu Thr Asp Ser Leu Thr Leu Gly Gln Gly His Ile Pro Val Ser Val	
115 120 125	
CCA GAT GAT CGA GCT GAA CAA CGA ACC TGT CTC ATC TGT GGC GAC CGC	432
Pro Asp Asp Arg Ala Glu Gln Arg Thr Cys Leu Ile Cys Gly Asp Arg	
130 135 140	
GCT ACG GGC TTG CAC TAT GGG ATC ATC TCC TGC GAG GGC TGC AAG GGC	480
Ala Thr Gly Leu His Tyr Gly Ile Ile Ser Cys Glu Gly Cys Lys Gly	
145 150 155 160	
TTT TTC AAG AGG AGC ATT TGC AAC AAA CGG GTG TAT CGG TGC AGT CGT	528
Phe Phe Lys Arg Ser Ile Cys Asn Lys Arg Val Tyr Arg Cys Ser Arg	
165 170 175	

GAC Asp	AAG Lys	AAC Asn	TGT Cys 180	GTC Val	ATG Met	TCC Ser	CGG Arg	AAG Lys 185	CAG Gln	AGG Arg	AAC Asn	AGA Arg	TGT Cys 190	CAG Gln	TAC Tyr	576
TGC Cys	CGC Arg	CTG Leu 195	CTC Leu	AAG Lys	TGT Cys	CTC Leu	CAG Gln 200	ATG Met	GGC Gly	ATG Met	AAC Asn	AGG Arg 205	AAG Lys	GCT Ala	ATC Ile	624
AGA Arg	GAA Glu 210	GAT Asp	GGC Gly	ATG Met	CCT Pro	GGA Gly 215	GGC Gly	CGG Arg	AAC Asn	AAG Lys	AGC Ser 220	ATT Ile	GGA Gly	CCA Pro	GTC Val	672
CAG Gln 225	ATA Ile	TCA Ser	GAA Glu	GAA Glu 230	GAA Glu	ATT Ile	GAA Glu	AGA Arg	ATC Ile	ATG Met 235	TCT Ser	GGA Gly	CAG Gln	GAG Glu	TTT Phe 240	720
GAG Glu	GAA Glu	GAA Glu	GCC Ala	AAT Asn 245	CAC His	TGG Trp	AGC Ser	AAC Asn	CAT His 250	GGT Gly	GAC Asp	AGC Ser	GAC Asp	CAC His 255	AGT Ser	768
TCC Ser	CCT Pro	GGG Gly	AAC Asn 260	AGG Arg	GCT Ala	TCA Ser	GAG Glu	AGC Ser 265	AAC Asn	CAG Gln	CCC Pro	TCA Ser	CCA Pro 270	GGC Gly	TCC Ser	816
ACA Thr	CTA Leu 275	TCA Ser	TCC Ser	AGT Ser	AGG Arg	TCT Ser	GTG Val 280	GAA Glu	CTA Leu	AAT Asn	GGA Gly	TTC Phe 285	ATG Met	GCA Ala	TTC Phe	864
AGG Arg 290	GAT Asp	CAG Gln	TAC Tyr	ATG Met	GGG Gly	ATG Met 295	TCA Ser	GTG Val	CCT Pro	CCA Pro	CAT His 300	TAT Tyr	CAA Gln	TAC Tyr	ATA Ile	912
CCA Pro 305	CAC His	CTT Leu	TTT Phe	AGC Ser	TAT Tyr 310	TCT Ser	GGC Gly	CAC His	TCA Ser	CCA Pro 315	CTT Leu	TTG Leu	CCC Pro	CCA Pro	CAA Gln 320	960
GCT Ala	CGA Arg	AGC Ser	CTG Leu	GAC Asp 325	CCT Pro	CAG Gln	TCC Ser	TAC Tyr	AGT Ser 330	CTG Leu	ATT Ile	CAT His	CAG Gln	CTG Leu 335	ATG Met	1008
TCA Ser	GCC Ala	GAA Glu	GAC Asp 340	CTG Leu	GAG Glu	CCA Pro	TTG Leu	GGC Gly 345	ACA Thr	CCT Pro	ATG Met	TTG Leu	ATT Ile	GAA Glu	GAT Asp	1056
GGG Gly	TAT Tyr 355	GCT Ala	GTG Val	ACA Thr	CAG Gln	GCA Ala	GAA Glu 360	CTG Leu	TTT Phe	GCT Ala	CTG Leu	CTT Leu 365	TGC Cys	CGC Arg	CTG Leu	1104
GCC Ala 370	GAC Asp	GAG Glu	TTG Leu	CTC Leu	TTT Phe	AGG Arg 375	CAG Gln	ATT Ile	GCC Ala	TGG Trp	ATC Ile 380	AAG Lys	AAG Lys	CTG Leu	CCT Pro	1152
TTT Phe 385	TTT Phe	TGC Cys	GAG Glu	CTC Leu	TCA Ser 390	ATC Ile	AAG Lys	GAT Asp	TAC Tyr	ACG Thr 395	TGC Cys	CTC Leu	TTG Leu	AGC Ser	TCT Ser 400	1200
ACG Thr	TGG Trp	CAG Gln	GAG Glu	TTA Leu 405	ATC Ile	CTG Leu	CTC Leu	TCC Ser	TCC Ser 410	CTC Leu	ACA Thr	GTG Val	TAC Tyr	AGC Ser 415	AAG Lys	1248
CAG Gln	ATC Ile	TTT Phe	GGG Gly 420	GAG Glu	CTG Leu	GCT Ala	GAT Asp	GTG Val 425	ACA Thr	GCC Ala	AAG Lys	TAC Tyr	TCA Ser	CCC Pro	TCT Ser r	1296
GAT Asp	GAA Glu 435	GAA Glu	CTC Leu	CAC His	AGA Arg	TTT Phe	AGT Ser 440	GAT Asp	GAA Glu	GGG Gly	ATG Met	GAG Glu 445	GTG Val	ATT Ile	CAA Glu	1344

CGA	CTC	ATC	TAC	CTA	TAT	CAG	AAG	TTC	CAT	CAG	CTG	AAG	GTC	AGC	AAC	
Arg	Leu	Ile	Tyr	Leu	Tyr	His	Lys	Phe	His	Gln	Leu	Lys	Val	Ser	Asn	
450						455					460					
																1392
GAG	GAG	TAC	GCA	TGC	ATG	AAA	GCA	ATT	AAC	TTC	CTG	AAT	CAA	GAT	ATC	
Glu	Glu	Tyr	Ala	Cys	Met	Lys	Ala	Ile	Asn	Phe	Leu	Asn	Gln	Asp	Ile	
465					470					475					480	
																1440
AGG	GGT	CTG	ACC	AGT	GCC	TCA	CAG	CTG	GAA	CAA	CTG	AAC	AAG	CGG	TAT	
Arg	Gly	Leu	Thr	Ser	Ala	Ser	Gln	Leu	Glu	Gln	Leu	Asn	Lys	Arg	Tyr	
				485					490					495		
																1488
TGG	TAC	ATT	TGT	CAG	GAT	TTC	ACT	GAA	TAT	AAA	TAC	ACA	CAT	CAG	CCA	
Trp	Tyr	Ile	Cys	Gln	Asp	Phe	Thr	Glu	Tyr	Lys	Tyr	Thr	His	Gln	Pro	
			500					505					510			
																1536
AAC	CGC	TTT	CCT	GAT	CTT	ATG	ATG	TGC	TTG	CCA	GAG	ATC	CGA	TAC	ATC	
Asn	Arg	Phe	Pro	Asp	Leu	Met	Met	Cys	Leu	Pro	Glu	Ile	Arg	Tyr	Ile	
		515					520					525				
																1584
GCA	GGC	AAG	ATG	GTG	AAT	GTG	CCC	CTG	GAG	CAG	CTG	CCC	CTC	CTC	TTT	
Ala	Gly	Lys	Met	Val	Asn	Val	Pro	Leu	Glu	Gln	Leu	Pro	Leu	Leu	Phe	
	530					535					540					
																1632
AAG	GTG	GTG	CTG	CAC	TCC	TGC	AAG	ACA	AGT	ACG	GTG	AAG	GAG	TGACCTGTGC		
Lys	Val	Val	Leu	His	Ser	Cys	Lys	Thr	Ser	Thr	Val	Lys	Glu			
545					550					555						
																1684
CCTGCACCTC CTTCGGGCCAC CCACAGT GCC TTGGGTAGGC AGCACAGGCT CCAGAGGAAA																1744
GAGCCAGAGA CCAAGATGGA GACTGTGGAG CAGCTACCTC CATCACAAGA AGAATTTGTT																1804
TGTTTTGTCTG TTTTAAACCT CATTTTTCTA TATATTTATT TCACGACAGA GTTGAATGTA																1864
TGGCCTTCAA CATGATGCAC ATGCTTTTGT GTGAATGCAG CAGATGCATT TCCTTGCACT																1924
TTACAGAATG TGAAGATGTT TAAIGTTACC GTGTTGTCAT TGTTTAGAGA TAGGTTTTTT																1984
TGTATTTTGA TGGAGAGGGT AGGATGGACT AGATGAGTAT TTCCATAATG TTGACAAAGA																2044
CAACTACCTC AATGGAACA CGTGTATGAC CATCCCTACC TTTTCCACA TTTTCTCAGC																2104
AGATACACAC TTGTCTGTIA GAGAGCAAAC TGCCTTTTTT ATAGCCACAG ACTTCTAAGT																2164
AAAAGAAGCA AACAAAGGAG CGAAGTGGA TAGGGAGATT TACTAATGGC CAGTTGGGAC																2224
ATCTGAGAGG CAATTTGATT TTGATCATCT CATCCCACAA GCCTGAAGGC AGAACTCTG																2284
CCTIACCTTC TGCTGCACCC CTCCTCCCCC CCACAGGCTG TTGTCTGTTG ATGCTGCTGT																2344
CAAGTTTTICA TCCAGGTAGA GTCCTAACAA TAAGCCAGTA TGTAGGACTT GCCTCCACGC																2404
GCCCTTGTAG CTCATAGCTG CCTAGTTTGC TGTICTAGAT CTACCAAGGC CTACTTCGGA																2464
ATTC																2468

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Phe Arg Arg Gly Gly Ala Arg Arg Glu Gly Pro Glu Pro Gly Gly
 1 5 10 15
 Ser Gly Ala Gln Arg Val Arg Arg Pro Arg Ala Cys Arg Pro Leu Thr
 20 25 30
 Ala Pro Ser Pro Arg Gly Arg Pro Gly Arg Arg Leu Arg Arg Arg Lys
 35 40 45
 Ser Trp Arg Ser Ser Glu Arg Arg Glu Gly Pro Glu His Arg Arg Met
 50 55 60
 Glu Arg Asp Glu Arg Pro Pro Ser Gly Gly Gly Gly Gly Gly Ser
 65 70 75 80
 Ala Gly Phe Leu Glu Pro Pro Ala Ala Leu Pro Pro Pro Pro Arg Asn
 85 90 95
 Gly Phe Cys Gln Asp Glu Leu Ala Glu Leu Asp Pro Gly Thr Asn Gly
 100 105 110
 Glu Thr Asp Ser Leu Thr Leu Gly Gln Gly His Ile Pro Val Ser Val
 115 120 125
 Pro Asp Asp Arg Ala Glu Gln Arg Thr Cys Leu Ile Cys Gly Asp Arg
 130 135 140
 Ala Thr Gly Leu His Tyr Gly Ile Ile Ser Cys Glu Gly Cys Lys Gly
 145 150 155 160
 Phe Phe Lys Arg Ser Ile Cys Asn Lys Arg Val Tyr Arg Cys Ser Arg
 165 170 175
 Asp Lys Asn Cys Val Met Ser Arg Lys Gln Arg Asn Arg Cys Gln Tyr
 180 185 190
 Cys Arg Leu Leu Lys Cys Leu Gln Met Gly Met Asn Arg Lys Ala Ile
 195 200 205
 Arg Glu Asp Gly Met Pro Gly Gly Arg Asn Lys Ser Ile Gly Pro Val
 210 215 220
 Gln Ile Ser Glu Glu Glu Ile Glu Arg Ile Met Ser Gly Gln Glu Phe
 225 230 235 240
 Glu Glu Glu Ala Asn His Trp Ser Asn His Gly Asp Ser Asp His Ser
 245 250 255
 Ser Pro Gly Asn Arg Ala Ser Glu Ser Asn Gln Pro Ser Pro Gly Ser
 260 265 270
 Thr Leu Ser Ser Ser Arg Ser Val Glu Leu Asn Gly Phe Met Ala Phe
 275 280 285
 Arg Asp Gln Tyr Met Gly Met Ser Val Pr Pr His Tyr Gln Tyr Ile
 290 295 300

Pro His Leu Ph Ser Tyr Ser Gly His Ser Pro Leu Leu Pro Pr Gln
 305 310 315 320
 Ala Arg Ser Leu Asp Pro Gln Ser Tyr Ser Leu Il His Gln Leu Met
 325 330 335
 Ser Ala Glu Asp Leu Glu Pro Leu Gly Thr Pro Met Leu Ile Glu Asp
 340 345 350
 Gly Tyr Ala Val Thr Gln Ala Glu Leu Phe Ala Leu Leu Cys Arg Leu
 355 360 365
 Ala Asp Glu Leu Leu Phe Arg Gln Ile Ala Trp Ile Lys Lys Leu Pro
 370 375 380
 Phe Phe Cys Glu Leu Ser Ile Lys Asp Tyr Thr Cys Leu Leu Ser Ser
 385 390 395 400
 Thr Trp Gln Glu Leu Ile Leu Leu Ser Ser Leu Thr Val Tyr Ser Lys
 405 410 415
 Gln Ile Phe Gly Glu Leu Ala Asp Val Thr Ala Lys Tyr Ser Pro Ser
 420 425 430
 Asp Glu Glu Leu His Arg Phe Ser Asp Glu Gly Met Glu Val Ile Glu
 435 440 445
 Arg Leu Ile Tyr Leu Tyr His Lys Phe His Gln Leu Lys Val Ser Asn
 450 455 460
 Glu Glu Tyr Ala Cys Met Lys Ala Ile Asn Phe Leu Asn Gln Asp Ile
 465 470 475 480
 Arg Gly Leu Thr Ser Ala Ser Gln Leu Glu Gln Leu Asn Lys Arg Tyr
 485 490 495
 Trp Tyr Ile Cys Gln Asp Phe Thr Glu Tyr Lys Tyr Thr His Gln Pro
 500 505 510
 Asn Arg Phe Pro Asp Leu Met Met Cys Leu Pro Glu Ile Arg Tyr Ile
 515 520 525
 Ala Gly Lys Met Val Asn Val Pro Leu Glu Gln Leu Pro Leu Leu Phe
 530 535 540
 Lys Val Val Leu His Ser Cys Lys Thr Ser Thr Val Lys Glu
 545 550 555

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: XR79 (XR79.SEQ)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 204..2009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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GCGTTAGAAA AGGTTCAAAA TAGGCACAAA GTCGTAAAAA TATCGTAACT GACCCGAAGT      60
AACATAACTT TAACCAAGTG CCTCGAAAAA TAGATGTTTT TAAAAGCTCA AGAATGGTGA      120
TAACAGACGT CCAATAAGAA TTTTCAAAGA GCCAATTATT TATACAGCCG ACGACTATTT      180
TTTAGCCGCC TGCTGTGCCG ACA ATG GAC GGC GTT AAG GTT GAG ACG TTC      230
                        Met Asp Gly Val Lys Val Glu Thr Phe
                        1                      5

ATC AAA AGC GAA GAA AAC CGA GCG ATG CCC TTG ATC GGA GGA GGC AGT      278
Ile Lys Ser Glu Glu Asn Arg Ala Met Pro Leu Ile Gly Gly Gly Ser
 10                      15                      20                      25

GCC TCA GGC GGC ACT CCT CTG CCA GGA GGC GGC GTG GGA ATG GCA GCC      326
Ala Ser Gly Gly Thr Pro Leu Pro Gly Gly Gly Val Gly Met Gly Ala
                      30                      35                      40

GGA GCA TCC GCA ACG TTG AGC GTG GAG CTG TGT TTG GTG TGC GGC GAC      374
Gly Ala Ser Ala Thr Leu Ser Val Glu Leu Cys Leu Val Cys Gly Asp
                      45                      50                      55

CGC GCC TCC GGC CCG CAC TAC GGA GCC ATA AGC TGC GAA GGC TGC AAG      422
Arg Ala Ser Gly Arg His Tyr Gly Ala Ile Ser Cys Glu Gly Cys Lys
                      60                      65                      70

GGA TTC TTC AAG CGC TCG ATC CGG AAG CAG CTG GGC TAC CAG TGT CGC      470
Gly Phe Phe Lys Arg Ser Ile Arg Lys Gln Leu Gly Tyr Gln Cys Arg
                      75                      80                      85

GGG GCT ATG AAC TGC GAG GTC ACC AAG CAC CAC AGG AAT CGG TGC CAG      518
Gly Ala Met Asn Cys Glu Val Thr Lys His His Arg Asn Arg Cys Gln
                      90                      95                      100                      105

TTC TGT CGA CTA CAG AAG TGC CTG GCC AGC GGC ATG CGA AGT GAT TCT      566
Phe Cys Arg Leu Gln Lys Cys Leu Ala Ser Gly Met Arg Ser Asp Ser
                      110                      115                      120

GTG CAG CAC GAG AGG AAA CCG ATT GTG CAC AGG AAG GAG GGC ATC ATC      614
Val Gln His Glu Arg Lys Pro Ile Val Asp Arg Lys Glu Gly Ile Ile
                      125                      130                      135

GCT GCT GCC GGT AGC TCA TCC ACT TCT GGC GGC GGT AAT GCC TCG TCC      662
Ala Ala Ala Gly Ser Ser Ser Thr Ser Gly Gly Gly Asn Gly Ser Ser
                      140                      145                      150

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ACC TAC CTA TCC GGC AAG TCC GGC TAT CAG CAG GGG CGT GGC AAG GGG Thr Tyr Leu Ser Gly Lys Ser Gly Tyr Gln Gln Gly Arg Gly Lys Gly 155 160 165	710
CAC AGT GTA AAG GCC GAA TCC GCG CCA CGC CTC CAG TGC ACA GCG CGC His Ser Val Lys Ala Glu Ser Ala Pro Arg Leu Gln Cys Thr Ala Arg 170 175 180 185	758
CAG CAA CGG GCC TTC AAT TTG AAT GCA GAA TAT ATT CCG ATG GGT TTG Gln Gln Arg Ala Phe Asn Leu Asn Ala Glu Tyr Ile Pro Met Gly Leu 190 195 200	806
AAT TTC GCA GAA CTA ACG CAG ACA TTG ATG TTC GCT ACC CAA CAG CAG Asn Phe Ala Glu Leu Thr Gln Thr Leu Met Phe Ala Thr Gln Gln Gln 205 210 215	854
CAG CAA CAA CAG CAA CAG CAT CAA CAG AGT GGT AGC TAT TCG CCA GAT Gln Gln Gln Gln Gln His Gln Gln Ser Gly Ser Tyr Ser Pro Asp 220 225 230	902
ATT CCG AAG GCA GAT CCC GAG GAT GAC GAG GAC GAC TCA ATG GAC AAC Ile Pro Lys Ala Asp Pro Glu Asp Asp Glu Asp Asp Ser Met Asp Asn 235 240 245	950
AGC AGC ACG CTG TGC TTG CAG TTG CTC GCC AAC AGC GCC AGC AAC AAC Ser Ser Thr Leu Cys Leu Gln Leu Leu Ala Asn Ser Ala Ser Asn Asn 250 255 260 265	998
AAC TCG CAG CAC CTG AAC TTT AAT GCT GGG GAA GTA CCC ACC GCT CTG Asn Ser Gln His Leu Asn Phe Asn Ala Gly Glu Val Pro Thr Ala Leu 270 275 280	1046
CCT ACC ACC TCG ACA ATG GGG CTT ATT CAG AGT TCG CTG GAC ATG CCG Pro Thr Thr Ser Thr Met Gly Leu Ile Gln Ser Ser Leu Asp Met Arg 285 290 295	1094
GTC ATC CAC AAG GGA CTG CAG ATC CTG CAG CCC ATC CAA AAC CAA CTG Val Ile His Lys Gly Leu Gln Ile Leu Gln Pro Ile Gln Asn Gln Leu 300 305 310	1142
GAG CGA AAT GGT AAT CTG AGT GTG AAG CCC GAG TGC GAT TCA GAG GCG Glu Arg Asn Gly Asn Leu Ser Val Lys Pro Glu Cys Asp Ser Glu Ala 315 320 325	1190
GAG GAC AGT GGC ACC GAG GAT GCC GTA GAC GCG GAG CTG GAG CAC ATG Glu Asp Ser Gly Thr Glu Asp Ala Val Asp Ala Glu Leu Glu His Met 330 335 340 345	1238
GAA CTA GAC TTT GAG TGC GGT GGG AAC CGA AGC GGT GGA AGC GAT TTT Glu Leu Asp Phe Glu Cys Gly Gly Asn Arg Ser Gly Gly Ser Asp Phe 350 355 360	1286
GCT ATC AAT GAG GCG GTC TTT GAA CAG GAT CTT CTC ACC GAT GTG CAG Ala Ile Asn Glu Ala Val Phe Glu Gln Asp Leu Leu Thr Asp Val Gln 365 370 375	1334
TGT GCC TTT CAT GTG CAA CCG CCG ACT TTG GTC CAG TCG TAT TTA AAT Cys Ala Phe His Val Gln Pro Pro Thr Leu Val His Ser Tyr Leu Asn 380 385 390	1382
ATT CAT TAT GTG TGT GAG ACG GGC TCG CGA ATC ATT TTT CTC ACC ATC Ile His Tyr Val Cys Glu Thr Gly Ser Arg Ile Ile Phe Leu Thr Ile 395 400 405	1430
CAT ACC CTT CGA AAG GTT CCA GTT TTC GAA CAA TTG GAA GCC CAT ACA His Thr Leu Arg Lys Val Pro Val Phe Glu Gln Leu Glu Ala His Thr 410 415 420 425	1478

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Asp Gly Val Lys Val Glu Thr Phe Ile Lys Ser Glu Glu Asn Arg
 1           5           10           15
Ala Met Pro Leu Ile Gly Gly Gly Ser Ala Ser Gly Gly Thr Pro Leu
          20           25           30
Pro Gly Gly Gly Val Gly Met Gly Ala Gly Ala Ser Ala Thr Leu Ser
          35           40           45
Val Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Arg His Tyr
          50           55           60
Gly Ala Ile Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser Ile
 65           70           75           80
Arg Lys Gln Leu Gly Tyr Gln Cys Arg Gly Ala Met Asn Cys Glu Val
          85           90           95
Thr Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Gln Lys Cys
          100          105          110
Leu Ala Ser Gly Met Arg Ser Asp Ser Val Gln His Glu Arg Lys Pro
          115          120          125
Ile Val Asp Arg Lys Glu Gly Ile Ile Ala Ala Ala Gly Ser Ser Ser
          130          135          140
Thr Ser Gly Gly Gly Asn Gly Ser Ser Thr Tyr Leu Ser Gly Lys Ser
          145          150          155          160
Gly Tyr Gln Gln Gly Arg Gly Lys Gly His Ser Val Lys Ala Glu Ser
          165          170          175
Ala Pro Arg Leu Gln Cys Thr Ala Arg Gln Gln Arg Ala Phe Asn Leu
          180          185          190
Asn Ala Glu Tyr Ile Pro Met Gly Leu Asn Phe Ala Glu Leu Thr Gln
          195          200          205
Thr Leu Met Phe Ala Thr Gln Gln Gln Gln Gln Gln Gln Gln His
          210          215          220
Gln Gln Ser Gly Ser Tyr Ser Pro Asp Ile Pro Lys Ala Asp Pro Glu
          225          230          235          240
Asp Asp Glu Asp Asp Ser Met Asp Asn Ser Ser Thr Leu Cys Leu Gln
          245          250          255
Leu Leu Ala Asn Ser Ala Ser Asn Asn Asn Ser Gln His Leu Asn Phe
          260          265          270
Asn Ala Gly Glu Val Pro Thr Ala Leu Pro Thr Thr Ser Thr Met Gly
          275          280          285
Leu Ile Gln Ser Ser Leu Asp Met Arg Val Ile His Lys Gly Leu Gln
          290          295          300

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Ile Leu Gln Pro Ile Gln Asn Gln Leu Glu Arg Asn Gly Asn Leu Ser
 305 310 315 320
 Val Lys Pro Glu Cys Asp S r Glu Ala Glu Asp Ser Gly Thr Glu Asp
 325 330 335
 Ala Val Asp Ala Glu Leu Glu His Met Glu Leu Asp Phe Glu Cys Gly
 340 345 350
 Gly Asn Arg Ser Gly Gly Ser Asp Phe Ala Ile Asn Glu Ala Val Phe
 355 360 365
 Glu Gln Asp Leu Leu Thr Asp Val Gln Cys Ala Phe His Val Gln Pro
 370 375 380
 Pro Thr Leu Val His Ser Tyr Leu Asn Ile His Tyr Val Cys Glu Thr
 385 390 395 400
 Gly Ser Arg Ile Ile Phe Leu Thr Ile His Thr Leu Arg Lys Val Pro
 405 410 415
 Val Phe Glu Gln Leu Glu Ala His Thr Gln Val Lys Leu Leu Arg Gly
 420 425 430
 Val Trp Pro Ala Leu Met Ala Ile Ala Leu Ala Gln Cys Gln Gly Gln
 435 440 445
 Leu Ser Val Pro Thr Ile Ile Gly Gln Phe Ile Gln Ser Thr Arg Gln
 450 455 460
 Leu Ala Asp Ile Asp Lys Ile Glu Pro Leu Lys Ile Ser Lys Met Ala
 465 470 475 480
 Asn Leu Thr Arg Thr Leu His Asp Phe Val Gln Glu Leu Gln Ser Leu
 485 490 495
 Asp Val Thr Asp Met Glu Phe Gly Leu Leu Arg Leu Ile Leu Leu Phe
 500 505 510
 Asn Pro Thr Leu Phe Gln His Arg Lys Glu Arg Ser Leu Arg Gly Tyr
 515 520 525
 Val Arg Arg Val Gln Leu Tyr Ala Leu Ser Ser Leu Arg Arg Gln Gly
 530 535 540
 Gly Ile Gly Gly Gly Glu Glu Arg Phe Asn Val Leu Val Ala Arg Leu
 545 550 555 560
 Leu Pro Leu Ser Ser Leu Asp Ala Glu Ala Met Glu Glu Leu Phe Phe
 565 570 575
 Ala Asn Leu Val Gly Gln Met Gln Met Asp Ala Leu Ile Pro Phe Ile
 580 585 590
 Leu Met Thr Ser Asn Thr Ser Gly Leu
 595 600

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That which is claimed is:

1. DNA encoding a polypeptide characterized by having a DNA binding domain comprising about 66 amino acids with 9 Cys residues, wherein said DNA binding domain has:

- 5 (i) less than about 70% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) less than about 60% amino acid sequence identity with the DNA binding domain of hTR-beta;
- 10 (iii) less than about 50% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) less than about 65% amino acid sequence identity with the DNA binding domain of hRXR-alpha.
- 15

2. DNA according to Claim 1 wherein the ligand binding domain of said polypeptide has:

- 20 (i) less than about 35% amino acid sequence identity with the ligand binding domain of hRAR-alpha;
- (ii) less than about 30% amino acid sequence identity with the ligand binding domain of hTR-beta;
- 25 (iii) less than about 25% amino acid sequence identity with the ligand binding domain of hGR; and
- (iv) less than about 30% amino acid sequence identity with the ligand binding domain of hRXR-alpha.
- 30

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3. DNA according to Claim 1 wherein said polypeptide has an overall amino acid sequence identity of:

- (i) less than about 35% relative to hRAR-alpha;
- 5 (ii) less than about 35% relative to hTR-beta;
- (iii) less than about 25% relative to hGR; and
- 10 (iv) less than about 35% relative to hRXR-alpha.

4. DNA according to Claim 1 wherein said polypeptide is characterized by having a DNA binding domain comprising [XR1]:

- 15 (i) about 68% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) about 59% amino acid sequence identity with the DNA binding domain of
- 20 hTR-beta;
- (iii) about 45% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) about 65% amino acid sequence identity with the DNA binding domain of
- 25 hRXR-alpha.

5. DNA according to Claim 1 wherein said polypeptide is characterized by having a DNA binding domain comprising [XR2]:

- 30 (i) about 55% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) about 56% amino acid sequence identity with the DNA binding domain of
- 35 hTR-beta;

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- (iii) about 50% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) about 52% amino acid sequence identity with the DNA binding domain of hRXR-alpha.

5

6. DNA according to Claim 1 wherein said polypeptide is characterized by having a DNA binding domain comprising [XR4]:

- 10 (i) about 62% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) about 58% amino acid sequence identity with the DNA binding domain of
- 15 hTR-beta;
- (iii) about 48% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) about 62% amino acid sequence identity with the DNA binding domain of
- 20 hRXR-alpha.

7. DNA according to Claim 1 wherein said polypeptide is characterized by having a DNA binding domain comprising [XR5]:

- 25 (i) about 59% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) about 52% amino acid sequence identity with the DNA binding domain of
- 30 hTR-beta;
- (iii) about 44% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) about 61% amino acid sequence identity with the DNA binding domain of
- 35 hRXR-alpha.

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8. DNA according to Claim 1 wherein said polypeptide is characterized by having a DNA binding domain comprising [XR79]:

- 5 (i) about 59% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) about 55% amino acid sequence identity with the DNA binding domain of hTR-beta;
- 10 (iii) about 50% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) about 65% amino acid sequence identity with the DNA binding domain of hRXR-alpha.

15

9. DNA according to Claim 1 wherein the nucleotide sequence of said DNA is selected from the nucleotide sequence set forth in Sequence ID No. 1, the combination of Sequence ID No. 3 and the continuation thereof as set forth in Sequence ID No. 1, the combination of Sequence ID No. 5 and the continuation thereof as set forth in Sequence ID No. 1, Sequence ID No. 7, Sequence ID No. 9, Sequence ID No. 11, or Sequence ID No. 13.

25 10. An expression vector comprising DNA according to claim 1, and further comprising:

at the 5'-end of said DNA, a promoter and a triplet encoding a translational start codon, and

30 at the 3'-end of said DNA, a triplet encoding a translational stop codon;

wherein said expression vector is operative in an animal cell in culture to express the protein encoded by the continuous sequence of amino acid-encoding triplets.

35 11. An animal cell in culture transformed with an expression vector according to Claim 10.

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12. A method of making a polypeptide comprising culturing the cells of Claim 11 under conditions suitable for the expression of said polypeptide.

5 13. The polypeptide produced by the method of Claim 12.

14. A polypeptide characterized by having a DNA binding domain comprising about 66 amino acids with 9 Cys
10 residues, wherein said DNA binding domain has:

- (i) less than about 70% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- 15 (ii) less than about 60% amino acid sequence identity with the DNA binding domain of hTR-beta;
- (iii) less than about 50% amino acid sequence identity with the DNA binding domain of hGR; and
- 20 (iv) less than about 65% amino acid sequence identity with the DNA binding domain of hRXR-alpha.

15. A DNA or RNA labeled for detection; wherein
25 said DNA or RNA comprises a nucleic acid segment of at least 20 bases in length, wherein said segment has substantially the same sequence as a segment of the same length selected from the DNA segment represented by bases 21 -1902, inclusive, of Sequence ID No. 1, bases 1 - 386,
30 inclusive, of Sequence ID No. 3, bases 10 - 300, inclusive, of Sequence ID No. 5, bases 21 - 1615, inclusive, of Sequence ID No. 7, bases 21 - 2000, inclusive, of Sequence ID No. 9, bases 1 - 2450, inclusive, of Sequence ID No. 11, bases 21 - 2295, inclusive, of Sequence ID No. 13, or the
35 complement of any one of said segments.

-63-

16. A method of testing a compound for its ability to regulate transcription-activating effects of a receptor polypeptide, said method comprising assaying for the presence or absence of reporter protein upon contacting
5 of cells containing a receptor polypeptide and reporter vector with said compound;

wherein said receptor polypeptide is characterized by having a DNA binding domain comprising about 66 amino acids with 9 Cys residues, wherein said DNA
10 binding domain has:

- (i) less than about 70% amino acid sequence identity with the DNA binding domain of hRAR-alpha;
- (ii) less than about 60% amino acid sequence
15 identity with the DNA binding domain of hTR-beta;
- (iii) less than about 50% amino acid sequence identity with the DNA binding domain of hGR; and
- (iv) less than about 65% amino acid sequence
20 identity with the DNA binding domain of hRXR-alpha; and

wherein said reporter vector comprises:

- (a) a promoter that is operable in said
25 cell,
- (b) a hormone response element, and
- (c) a DNA segment encoding a reporter protein,

wherein said reporter protein-encoding
30 DNA segment is operatively linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element
35 is operatively linked to said promoter for activation thereof.

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17. A chimeric receptor comprising at least an amino-terminal domain, a DNA-binding domain, and a ligand-binding domain,

5 wherein at least one of the domains thereof is derived from the polypeptide of Claim 13; and wherein at least one of the domains thereof is derived from at least one previously identified member of the steroid/thyroid superfamily of receptors.

10

18. DNA encoding the chimeric receptor of Claim 17.

19. A method to identify compounds which act as
15 ligands for receptor polypeptides according to Claim 13 comprising:

assaying for the presence or absence of reporter protein upon contacting of cells containing a chimeric form of said receptor polypeptide and reporter vector with said
20 compound;

wherein said chimeric form of said receptor polypeptide comprises the ligand binding domain of said receptor polypeptide and the amino-terminal and DNA-binding domains of at least one previously identified member of the
25 steroid/thyroid superfamily of receptors;

wherein said reporter vector comprises:

- (a) a promoter that is operable in said cell,
- (b) a hormone response element which is
30 responsive to the receptor from which the DNA-binding domain of said chimeric form of said receptor polypeptide is derived, and
- (c) a DNA segment encoding a reporter
35 protein,

-65-

wherein said reporter protein-
encoding DNA segment is operatively
linked to said promoter for
transcription of said DNA segment, and

5 wherein said hormone response
element is operatively linked to said
promoter for activation thereof, and
thereafter

selecting those compounds which induce or block
10 the production of reporter in the presence of said chimeric
form of said receptor polypeptide.

20. A method to identify response elements for
receptor polypeptides according to Claim 13 comprising:

15 assaying for the presence or absence of reporter
protein upon contacting of cells containing a chimeric form
of said receptor polypeptide and reporter vector with a
compound which is a known agonist or antagonist for the
receptor from which the ligand-binding domain of said
20 chimeric form of said receptor polypeptide is derived;

wherein said chimeric form of said receptor
polypeptide comprises the DNA-binding domain of the
receptor polypeptide and the amino-terminal and
ligand-binding domains of at least one previously
25 identified member of the steroid/thyroid superfamily of
receptors;

wherein said reporter vector comprises:

- 30 (a) a promoter that is operable in said
cell,
(b) a putative hormone response element,
and
(c) a DNA segment encoding a reporter
protein,

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wherein said reporter protein-
encoding DNA segment is operatively
linked to said promoter for
transcription of said DNA segment, and
5 wherein said hormone response
element is operatively linked to said
promoter for activation thereof; and
identifying those response elements for which the
production of reporter is induced or blocked in the
10 presence of said chimeric form of said receptor
polypeptide.

21. A method of testing a compound for its
ability to selectively regulate transcription-activating
15 effects of a specific receptor polypeptide, said method
comprising:

assaying for the presence or absence of reporter
protein upon contacting of cells containing said receptor
polypeptide and reporter vector with said compound;

20 wherein said receptor polypeptide is
characterized by being responsive to the presence of a
known ligand for said receptor to regulate the
transcription of associated gene(s);

wherein said reporter vector comprises:

- 25 (a) a promoter that is operable in said
cell,
(b) a hormone response element, and
(c) a DNA segment encoding a reporter
protein,

30 wherein said reporter protein-
encoding DNA segment is operatively
linked to said promoter for
transcription of said DNA segment, and

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wherein said hormone response element is operatively linked to said promoter for activation thereof; and

assaying for the presence or absence of reporter protein upon contacting of cells containing chimeric receptor polypeptide and reporter vector with said compound;

wherein said chimeric receptor polypeptide comprises the ligand binding domain of the receptor of Claim 13 and the DNA binding domain of said specific receptor; and thereafter selecting those compounds which induce or block the production of reporter in the presence of said specific receptor, but are substantially unable to induce or block the production of reporter in the presence of said chimeric receptor.

22. A method according to Claim 21 wherein said contacting is carried out in the further presence of at least one agonist for said specific receptor.

verht19

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352

1952

verht3

//////////383
349

1952

verht5

//////////300
352

1952

FIG. 1

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) ⁶ According to International Patent Classification (IPC) or to both National Classification and IPC Int.Cl. 5 C12N15/12; C12N15/62; C07K13/00; C12N5/10 C12Q1/68; C07K15/00														
II. FIELDS SEARCHED Minimum Documentation Searched? <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 25%;">Classification System</td> <td colspan="2">Classification Symbols</td> </tr> <tr> <td>Int.Cl. 5--</td> <td>C12N ;</td> <td>C07K ; C12Q</td> </tr> </table> Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched ⁸			Classification System	Classification Symbols		Int.Cl. 5--	C12N ;	C07K ; C12Q						
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Int.Cl. 5--	C12N ;	C07K ; C12Q												
III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹ <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <th style="width: 10%;">Category¹⁰</th> <th style="width: 70%;">Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²</th> <th style="width: 20%;">Relevant to Claim No.¹³</th> </tr> <tr> <td style="text-align: center;">Y</td> <td> WO,A,9 113 167 (LELAND STANFORD JUNIOR UNIVERSITY, US) 5 September 1991 See Page 67, Table 4 page 111, claims </td> <td style="text-align: center;">1-8, 10-22</td> </tr> <tr> <td style="text-align: center;">Y</td> <td> WO,A,9 112 258 (THE SALK INST. FOR BIOL. STUDIES, US) 22 August 1991 See Figure 1, claims </td> <td style="text-align: center;">1-8, 10-22</td> </tr> <tr> <td style="text-align: center;">Y</td> <td> WO,A,9 006 364 (THE SALK INSTITUTE FOR BIOLOGICAL STUDIES, US) 14 June 1990 see the whole document </td> <td style="text-align: center;">1-8, 10-20</td> </tr> </table>			Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³	Y	WO,A,9 113 167 (LELAND STANFORD JUNIOR UNIVERSITY, US) 5 September 1991 See Page 67, Table 4 page 111, claims	1-8, 10-22	Y	WO,A,9 112 258 (THE SALK INST. FOR BIOL. STUDIES, US) 22 August 1991 See Figure 1, claims	1-8, 10-22	Y	WO,A,9 006 364 (THE SALK INSTITUTE FOR BIOLOGICAL STUDIES, US) 14 June 1990 see the whole document	1-8, 10-20
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<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>¹⁰ Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"A" document member of the same patent family</p> </div> </div>														
IV. CERTIFICATION <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 50%;"> Date of the Actual Completion of the International Search <div style="text-align: center;">17 DECEMBER 1992</div> </td> <td style="width: 50%;"> Date of Mailing of this International Search Report <div style="text-align: center;">21 01. 93</div> </td> </tr> <tr> <td> International Searching Authority <div style="text-align: center;">EUROPEAN PATENT OFFICE</div> </td> <td> Signature of Authorized Officer <div style="text-align: center;">S.A. NAUCHE </div> </td> </tr> </table>			Date of the Actual Completion of the International Search <div style="text-align: center;">17 DECEMBER 1992</div>	Date of Mailing of this International Search Report <div style="text-align: center;">21 01. 93</div>	International Searching Authority <div style="text-align: center;">EUROPEAN PATENT OFFICE</div>	Signature of Authorized Officer <div style="text-align: center;">S.A. NAUCHE </div>								
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**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO. US 9207570
SA 64632**

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